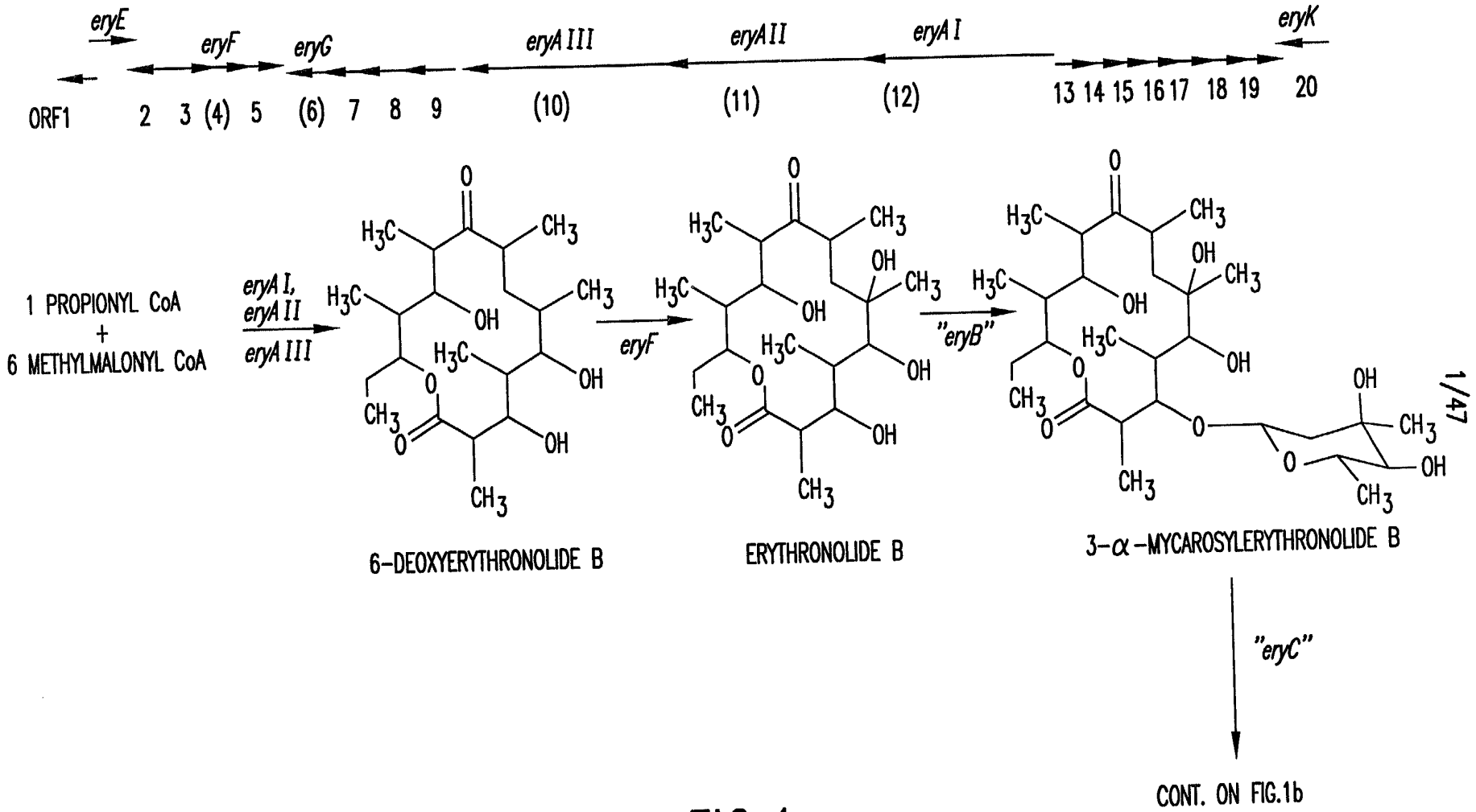


FIG.1a

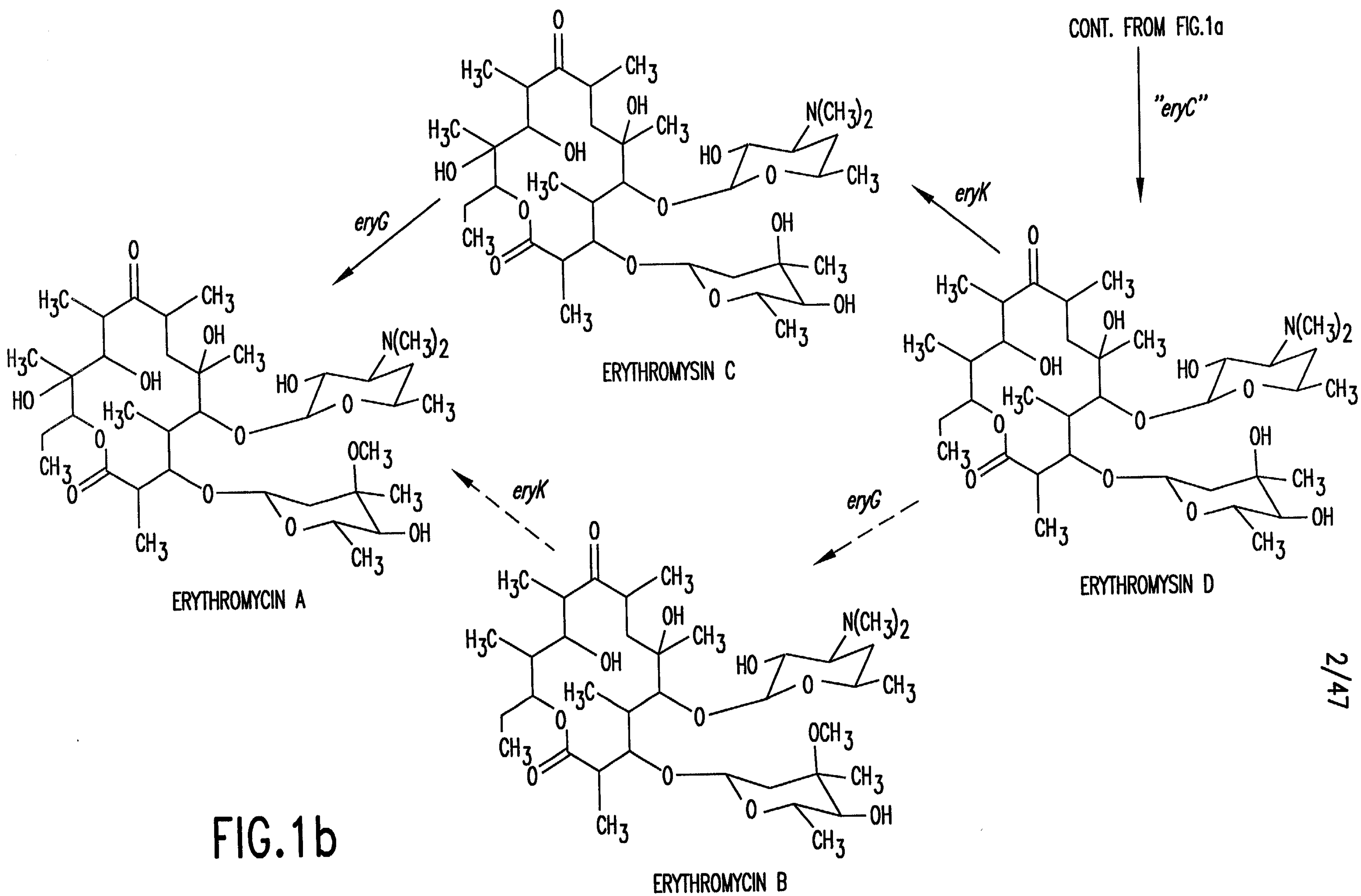

CONT. FROM FIG.1a
"eryC"
eryK
eryG
eryG
eryK
ERYTHROMYSIN D
ERYTHROMYSIN C
ERYTHROMYCIN B
ERYTHROMYCIN A

FIG.1b

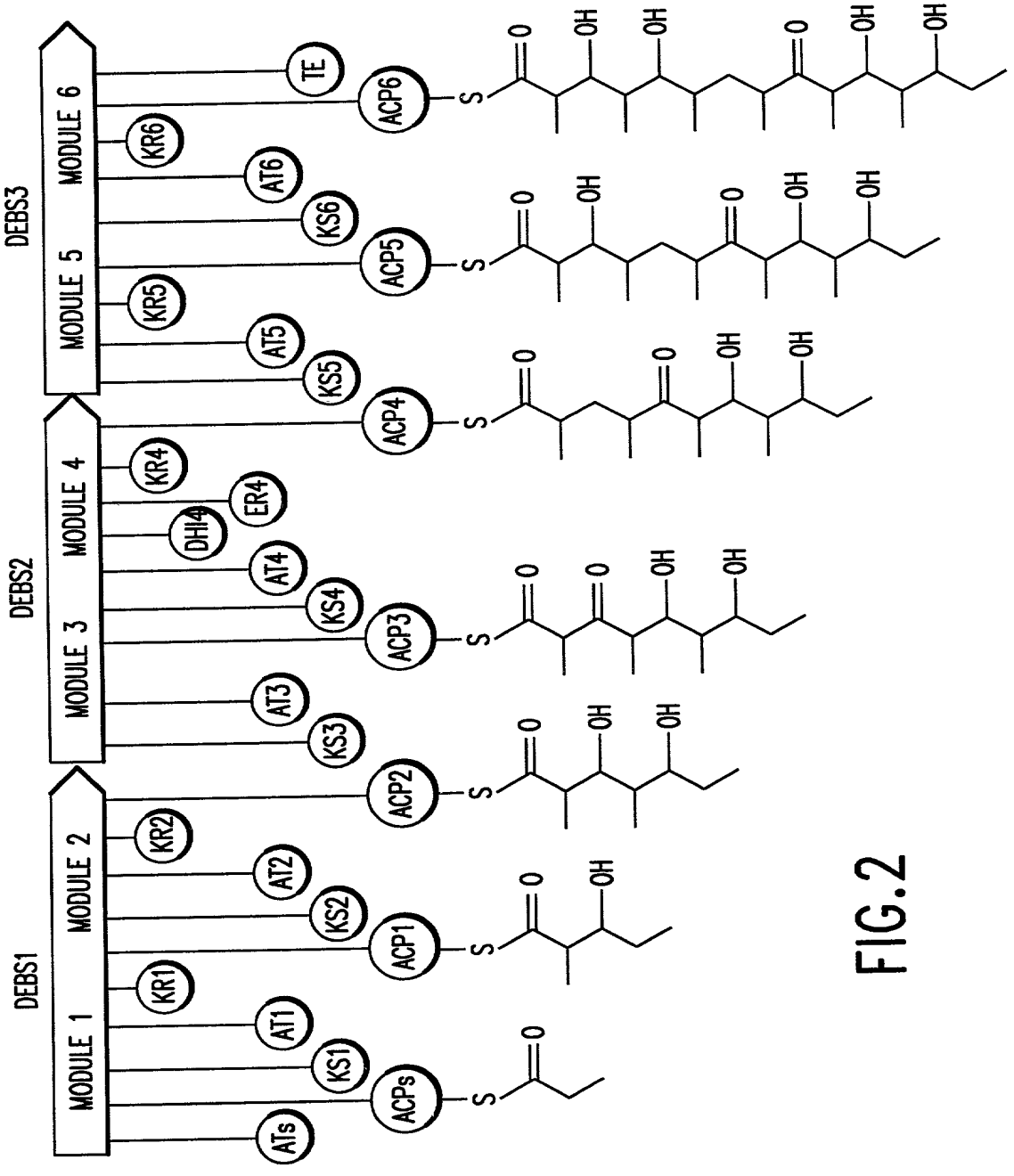

DEBS1
MODULE 1
MODULE 2
DEBS2
MODULE 3
MODULE 4
DEBS3
MODULE 5
MODULE 6
ATs
KS1
AT1
KR1
KS2
AT2
KR2
KS3
AT3
KS4
AT4
DH4
ER4
KR4
KS5
AT5
KR5
KS6
AT6
KR6
TE
ACPs
ACP1
ACP2
ACP3
ACP4
ACP5
ACP6
S
O
OH

FIG.2

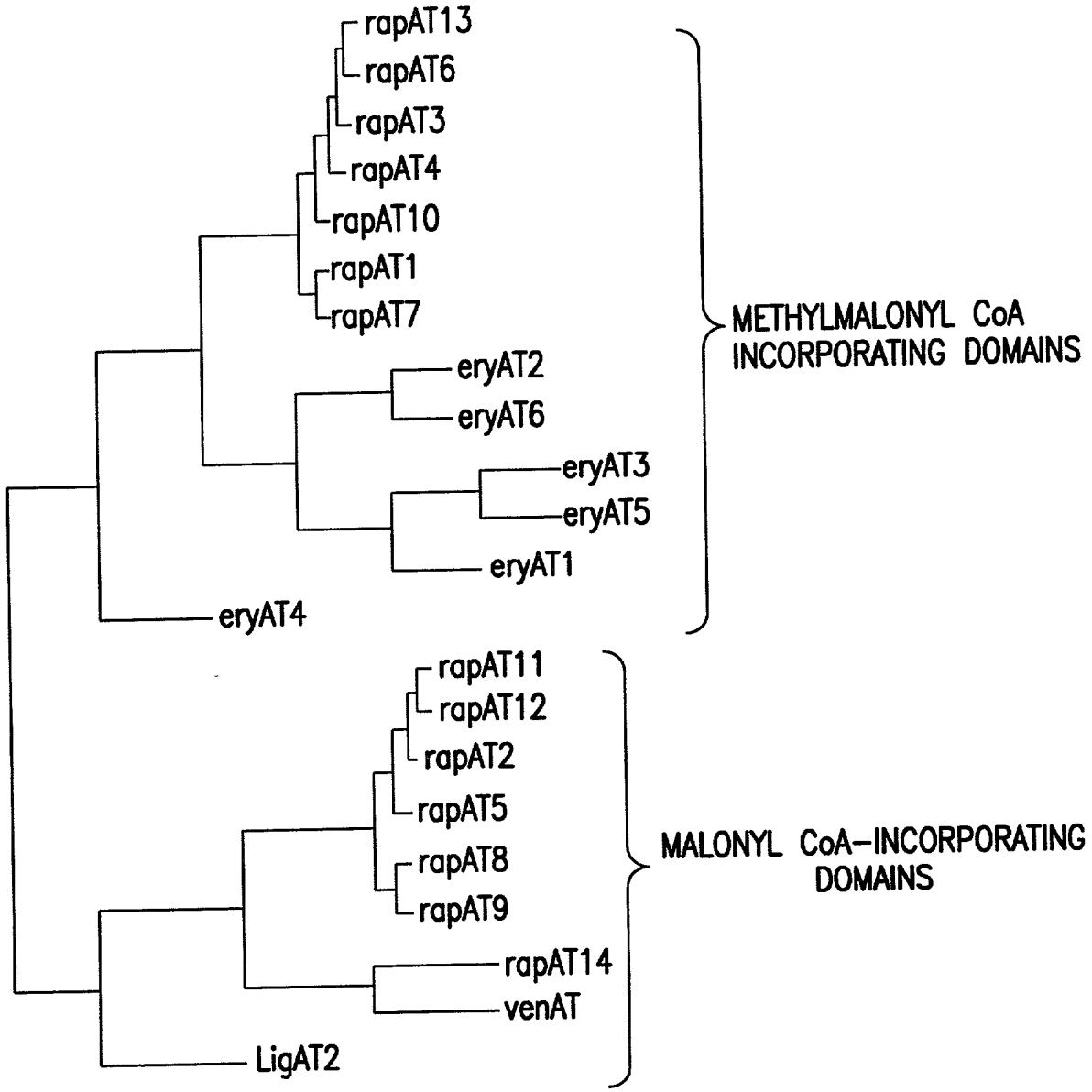

rapAT13
rapAT6
rapAT3
rapAT4
rapAT10
rapAT1
rapAT7
eryAT2
eryAT6
eryAT3
eryAT5
eryAT1
eryAT4
METHYLMALONYL CoA INCORPORATING DOMAINS
rapAT11
rapAT12
rapAT2
rapAT5
rapAT8
rapAT9
rapAT14
venAT
LigAT2
MALONYL CoA–INCORPORATING DOMAINS

FIG.3

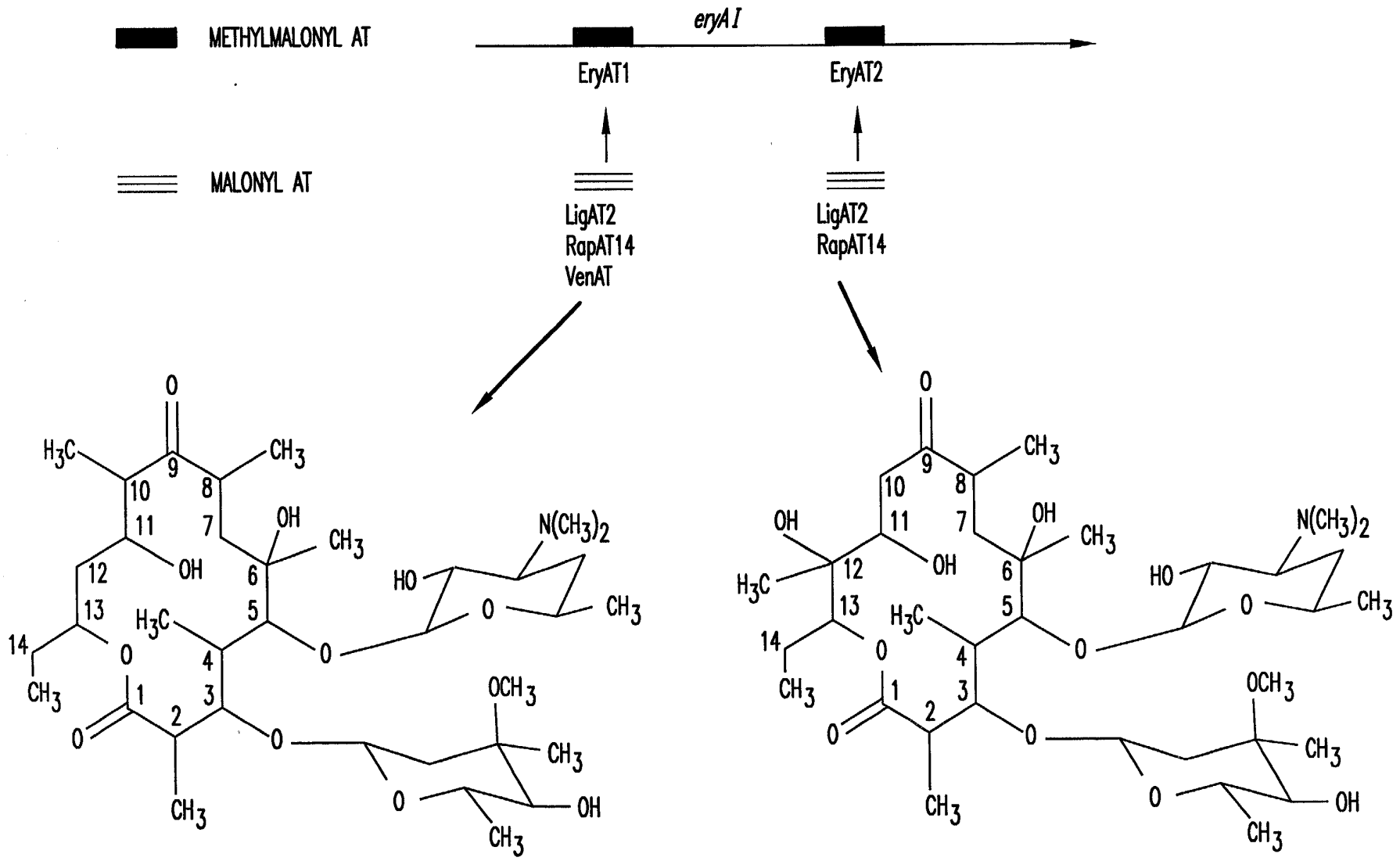
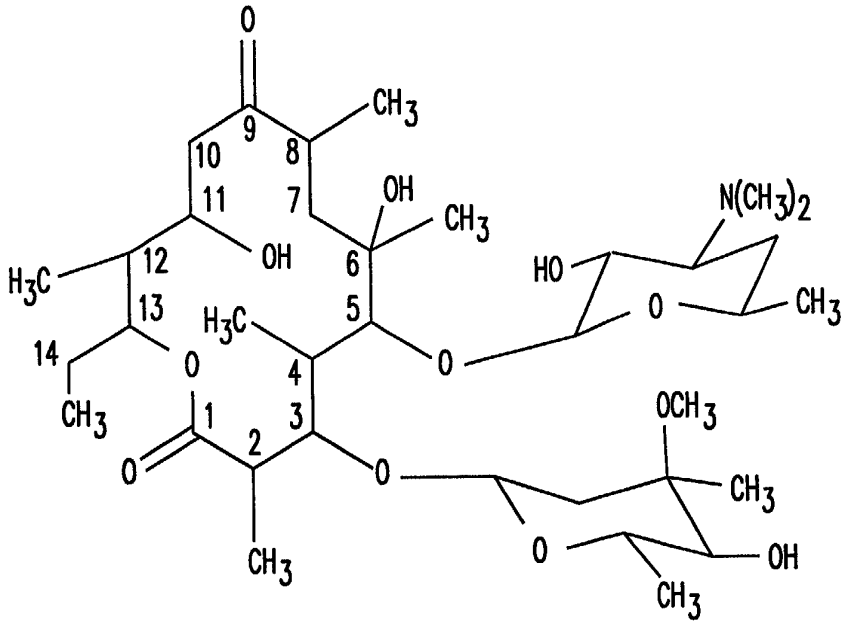

METHYLMALONYL AT
MALONYL AT
eryA I
EryAT1
EryAT2
LigAT2
RapAT14
VenAT
LigAT2
RapAT14
12-DESMETHYL, 12-DEOXYERYTHROMYCIN A
10-DESMETHYLERYTHROMYCIN A
AND
CONT. ON FIG.4b

FIG. 4a(1)

CONT. FROM FIG.4a



10-DESMETHYL-12-DEOXYERYTHROMYCIN A

FIG. 4a(2)

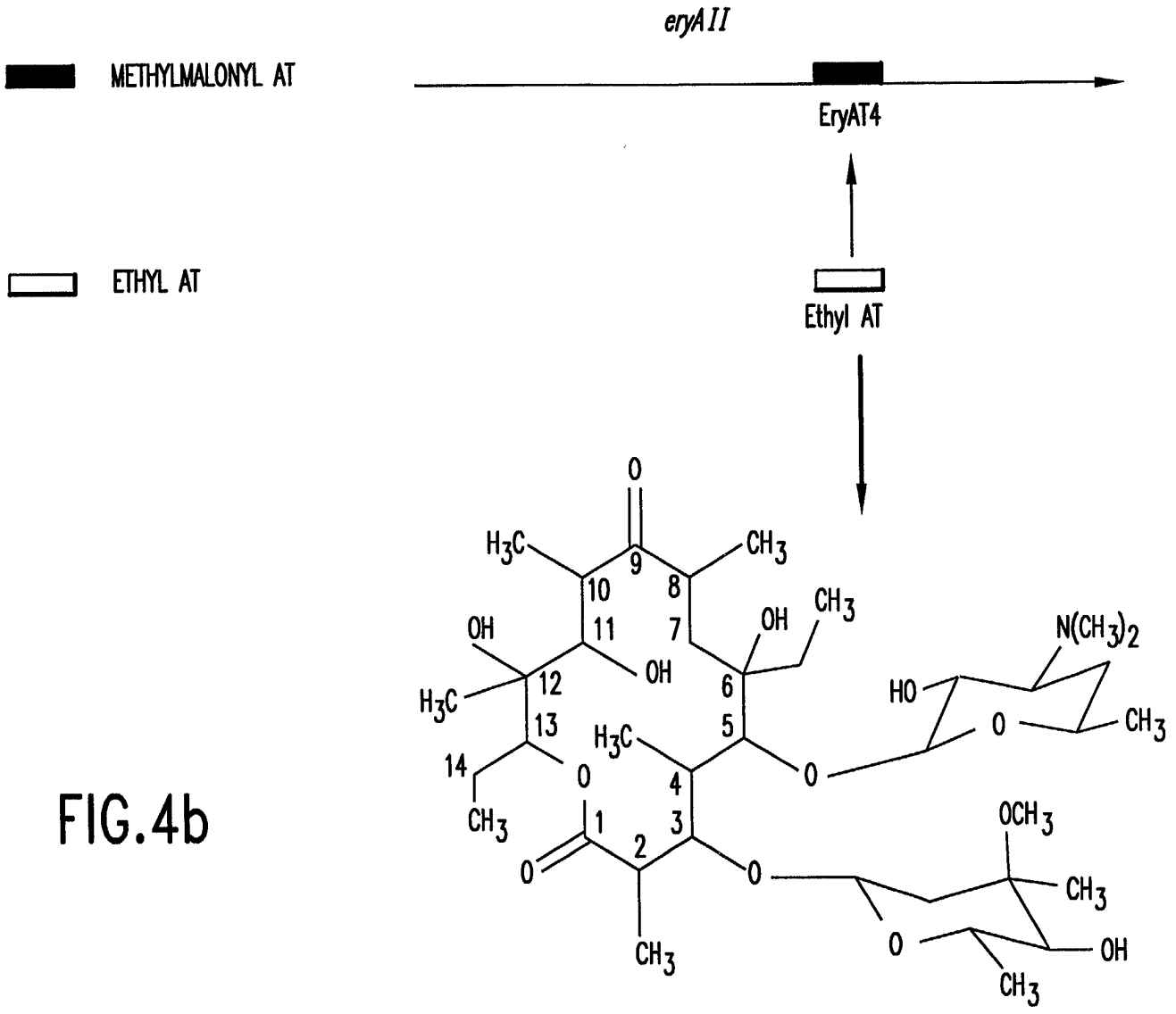

eryAII
METHYLMALONYL AT
ETHYL AT
EryAT4
Ethyl AT
6-DESMETHYL-6-ETHYLERYTHROMYSIN A

FIG.4b

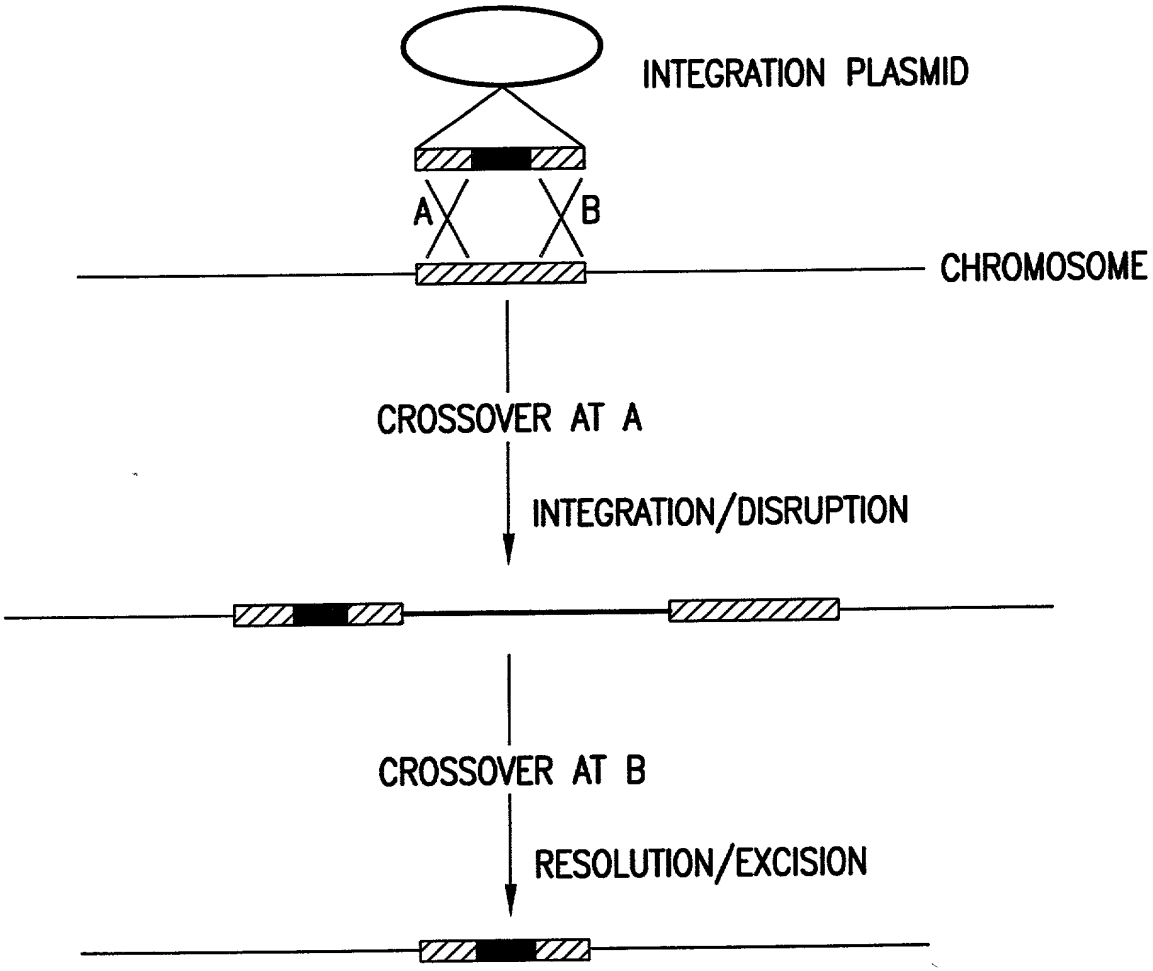

INTEGRATION PLASMID
A
B
CHROMOSOME
CROSSOVER AT A
INTEGRATION/DISRUPTION
CROSSOVER AT B
RESOLUTION/EXCISION

FIG.5

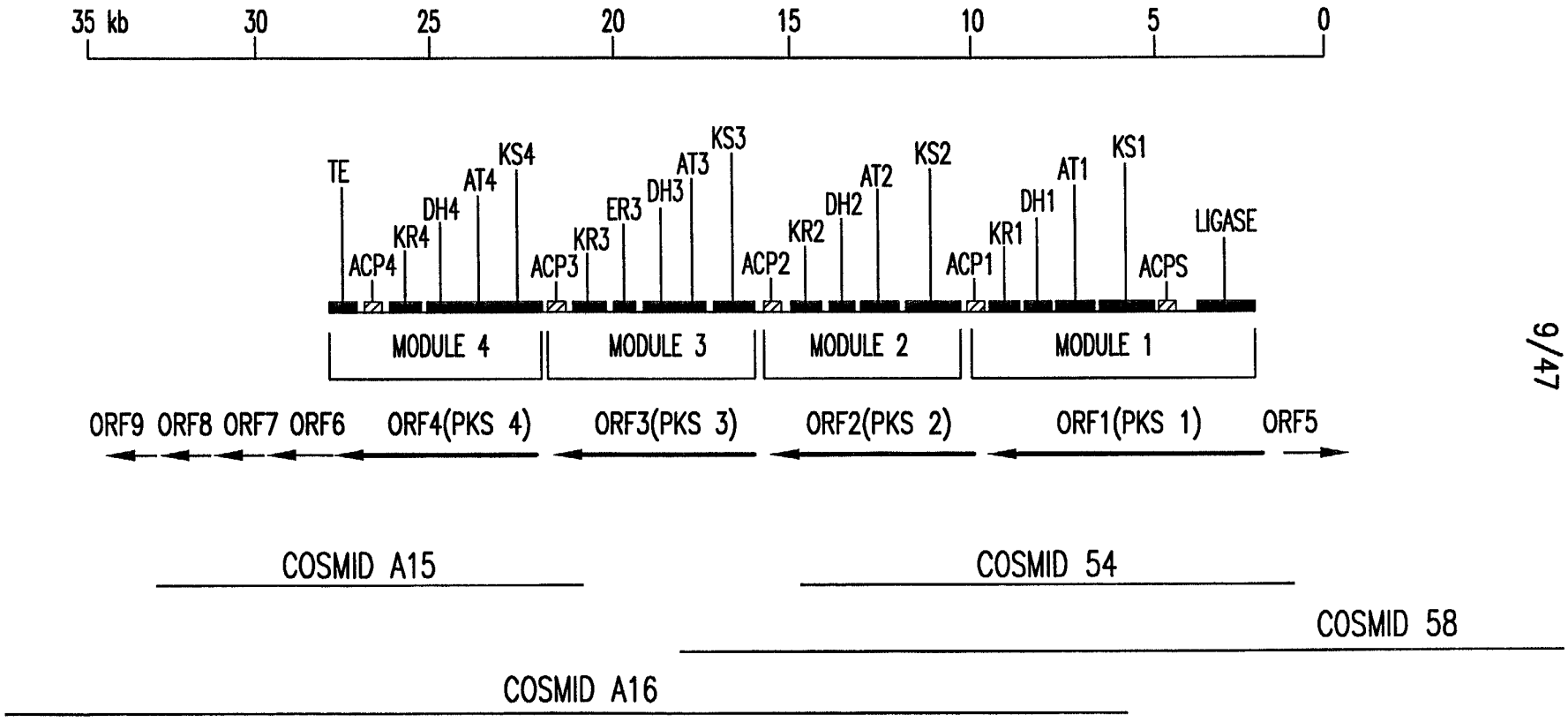
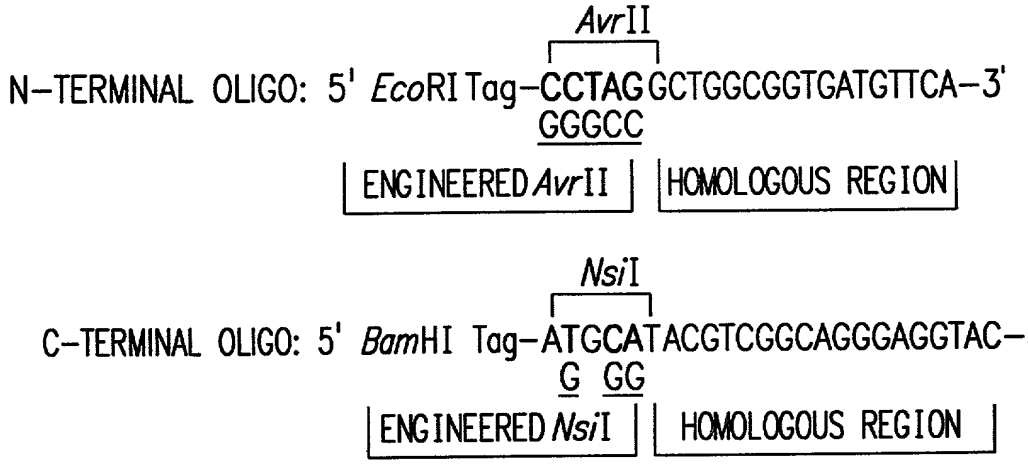

35 kb
30
25
20
15
10
5
0
TE
ACP4
KR4
DH4
AT4
KS4
ACP3
KR3
ER3
DH3
AT3
KS3
ACP2
KR2
DH2
AT2
KS2
ACP1
KR1
DH1
AT1
KS1
ACPS
LIGASE
MODULE 4
MODULE 3
MODULE 2
MODULE 1
ORF9 ORF8 ORF7 ORF6
ORF4(PKS 4)
ORF3(PKS 3)
ORF2(PKS 2)
ORF1(PKS 1)
ORF5
COSMID A15
COSMID 54
COSMID 58
COSMID A16

FIG.6

```
GGGCCGCTGGCGGTGATGTTCACCGGACAGGGCTCCCAACGCCCCGGCATGGGACGACAG  60
G  P  L  A  V  M  F  T  G  Q  G  S  Q  R  P  G  M  G  R  Q   20

TTGTACGAGCACTTCCCCGTCTSCGCCCAGGCACTGGACGAGGTCTTCGCACTCGCCACC  120
L  Y  E  H  F  P  V  F  A  Q  A  L  D  E  V  F  A  L  A  T   40

CCCGGACTACGCGAGGTGATGTTCGACCCCGACCAGGCCGAAACACTCCAACGCACCGAC  180
P  G  L  R  E  V  M  F  D  P  D  Q  A  E  T  L  Q  R  T  D   60

CACGCCCAGATCGCCCTGTTCGCCTTCGAAACCGCCCTCTACCGACTCTGGGAATCCTGG  240
H  A  Q  I  A  L  F  A  F  E  T  A  L  Y  R  L  W  E  S  W   80

GGCCTGCGACCCGACATGGTCTGCGGACACTCGGTCGGAGAAATCACCGCAGCCCACGTC  300
G  L  R  P  D  M  V  C  G  H  S  V  G  E  I  T  A  A  H  V   100

TCCGGCACCCTCACCCTCCCCGACGCCGTCCACCTCGTCACCACACGCGGCACCCTCATG  360
S  G  T  L  T  L  P  D  A  V  H  L  V  T  T  R  G  T  L  M   120

CAAAACCTGCCCCCCGGCGGCGCCATGCTCGCCGTCGCCACCGACCCCCACACCCTCCAA  420
Q  N  L  P  P  G  G  A  M  L  A  V  A  T  D  P  H  T  L  Q   140

CCCCACCTCGACAACCACCACGACACCATCTCCATCGCCGCCATCAACGGCCCCCACGCC  480
P  H  L  D  N  H  H  D  T  I  S  I  A  A  I  N  G  P  H  A   160

ACCGTCCTCTCCGGCGACCGCACCACCCTCCACCACATCGCCACCCAACTCAACACCAAA  540
T  V  L  S  G  D  R  T  T  L  H  H  I  A  T  Q  L  N  T  K   180

ACCAACTGGCTCAACGTCAGCCACGCCTTCCACTCCCCCCTCATGCAACCCATCCTCCAA  600
T  N  W  L  N  V  S  H  A  F  H  S  P  L  M  Q  P  I  L  Q   200

CCCTTCACCACCACCCTCAACACCCTCACCCACCACCCCCCACACACACCCCTCATCAGC  660
P  F  T  T  T  L  N  T  L  T  H  H  P  P  H  T  P  L  I  S   220

ATGCTCACCGCCACACCCACCCACCCCGACACCACCCACTGGACCCAGCACATCACCGCA  720
M  L  T  A  T  P  T  H  P  D  T  T  H  W  T  Q  H  I  T  A   240

CCCGTCCGCTACACCGACACCCTCCACCACCTCCACCACCACGGCATCACCACCTACCTC  780
P  V  R  Y  T  D  T  L  H  H  L  H  H  H  G  I  T  T  Y  L   260

GAAATCGGCCCCGACACCACCCTCACCGCCCTCGCCCGCACCACCCTCCCCACCACCACC  840
E  I  G  P  D  T  T  L  T  A  L  A  R  T  T  L  P  T  T  T   280

CACCTCATCCCCACCACCCGCCGCAACCACAACGAAGTCCGCAGCACGAACGAGGCGTTG  900
H  L  I  P  T  T  R  R  N  H  N  E  V  R  S  T  N  E  A  L   300

GGCAGGGTGTTCAGCGTGGGCCACTCGGTGGACTGGCGGGCCCTCACTCCGACCGGGAGG  960
G  R  V  F  S  V  G  H  S  V  D  W  R  A  L  T  P  T  G  R   320

CGTACCTCCCTGCCGACGTACCCCT                                     985
R  T  S  L  P  T  Y  P                                        328
```

FIG.7

PCR OLIGOS:



PCR CLONING:

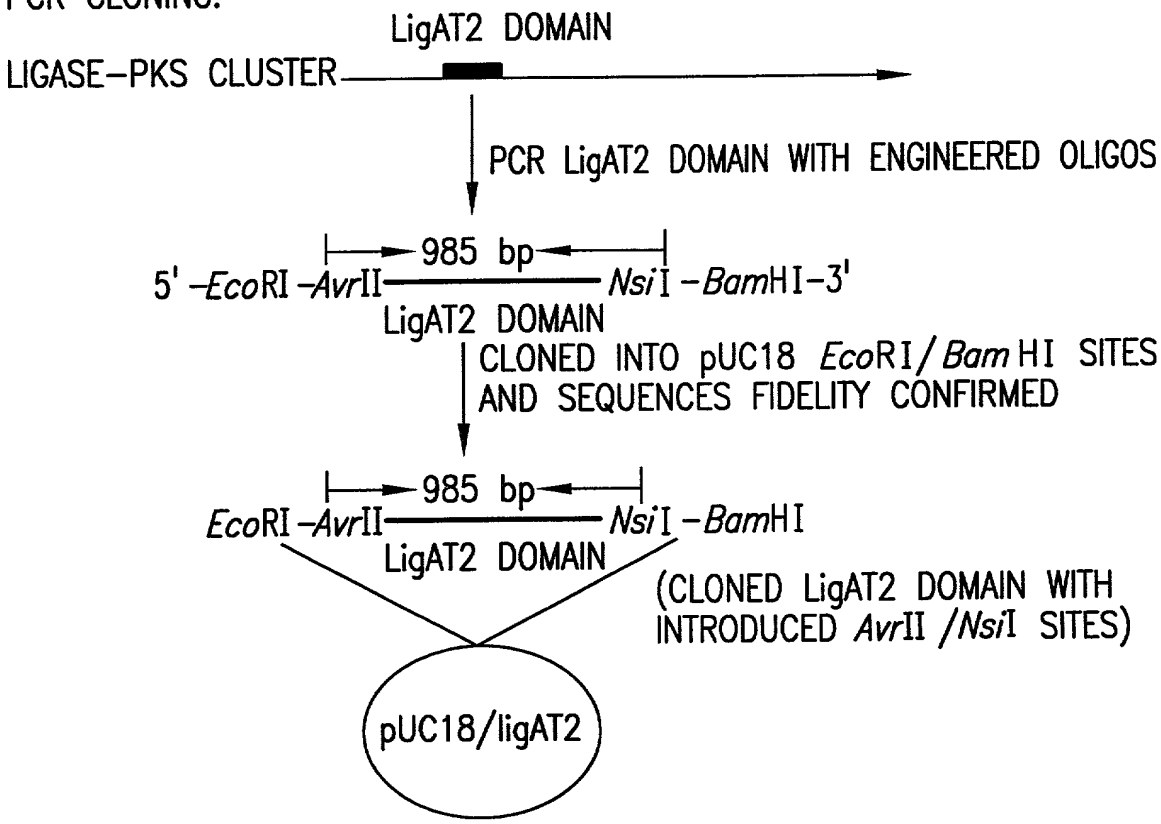


FIG.8

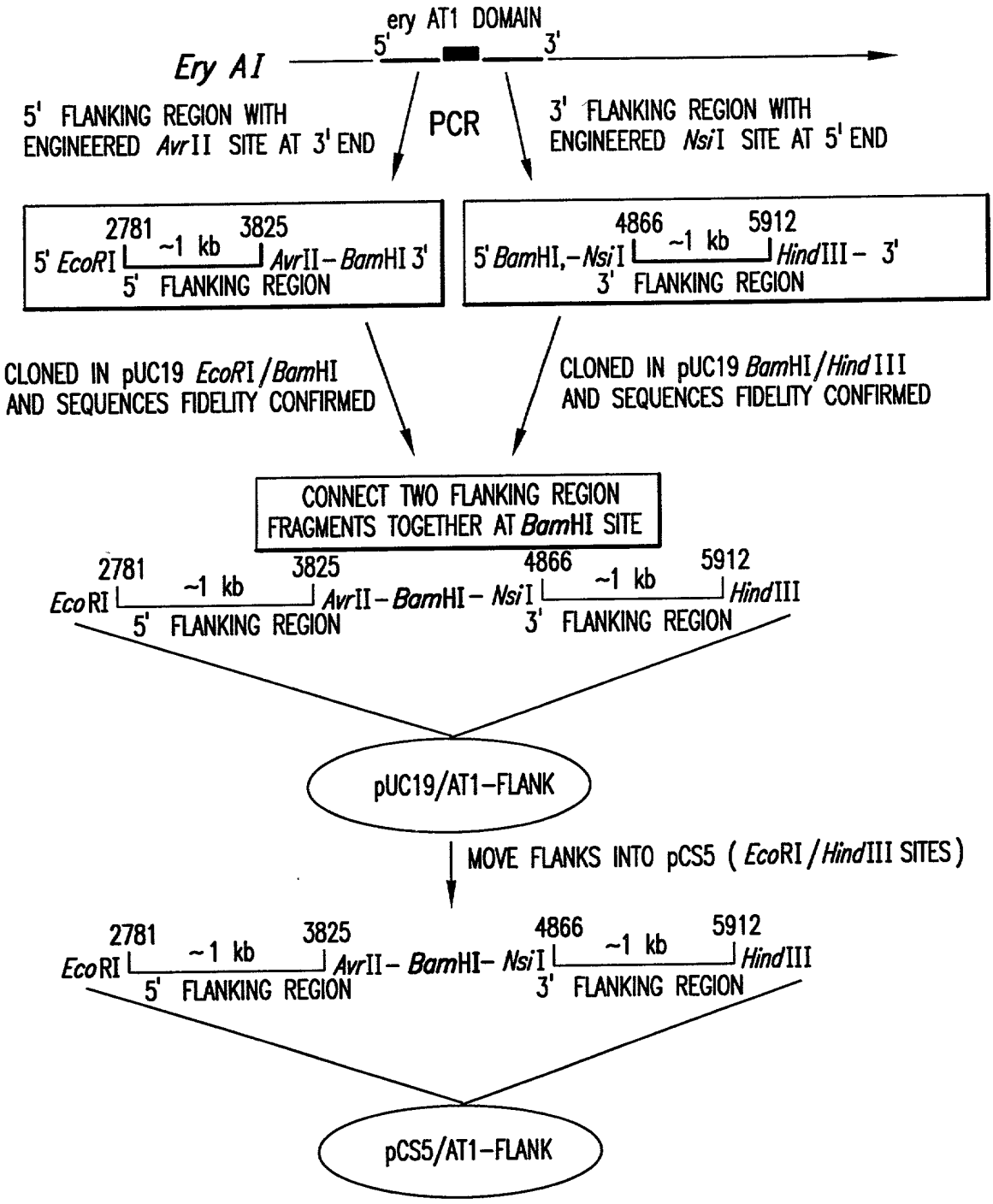

ery AT1 DOMAIN
5'
3'
Ery AI
5' FLANKING REGION WITH ENGINEERED AvrII SITE AT 3' END
PCR
3' FLANKING REGION WITH ENGINEERED NsiI SITE AT 5' END
2781
3825
5' EcoRI ~1 kb AvrII–BamHI 3'
5' FLANKING REGION
4866
5912
5' BamHI,–NsiI ~1 kb HindIII– 3'
3' FLANKING REGION
CLONED IN pUC19 EcoRI/BamHI AND SEQUENCES FIDELITY CONFIRMED
CLONED IN pUC19 BamHI/HindIII AND SEQUENCES FIDELITY CONFIRMED
CONNECT TWO FLANKING REGION FRAGMENTS TOGETHER AT BamHI SITE
2781
3825
4866
5912
EcoRI ~1 kb AvrII–BamHI– NsiI ~1 kb HindIII
5' FLANKING REGION
3' FLANKING REGION
pUC19/AT1–FLANK
MOVE FLANKS INTO pCS5 (EcoRI/HindIII SITES)
2781
3825
4866
5912
EcoRI ~1 kb AvrII– BamHI– NsiI ~1 kb HindIII
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT1–FLANK

FIG.9

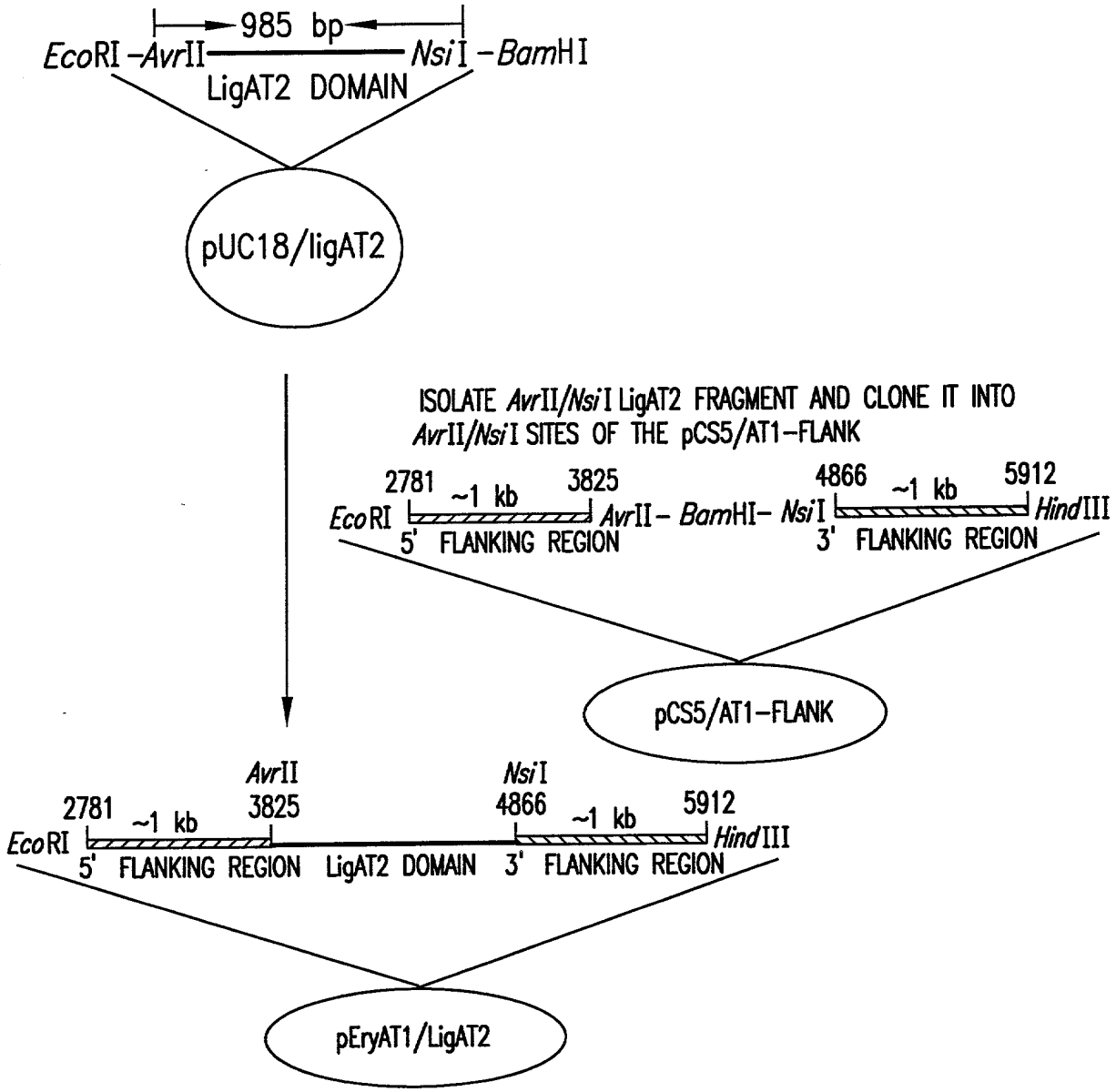

985 bp
EcoRI -AvrII- NsiI -BamHI
LigAT2 DOMAIN
pUC18/ligAT2
ISOLATE AvrII/NsiI LigAT2 FRAGMENT AND CLONE IT INTO
AvrII/NsiI SITES OF THE pCS5/AT1-FLANK
2781 ~1 kb 3825
EcoRI
5' FLANKING REGION
AvrII- BamHI- NsiI
4866 ~1 kb 5912
HindIII
3' FLANKING REGION
pCS5/AT1-FLANK
AvrII
NsiI
2781 ~1 kb 3825
4866 ~1 kb 5912
EcoRI
HindIII
5' FLANKING REGION
LigAT2 DOMAIN
3' FLANKING REGION
pEryAT1/LigAT2

FIG.10

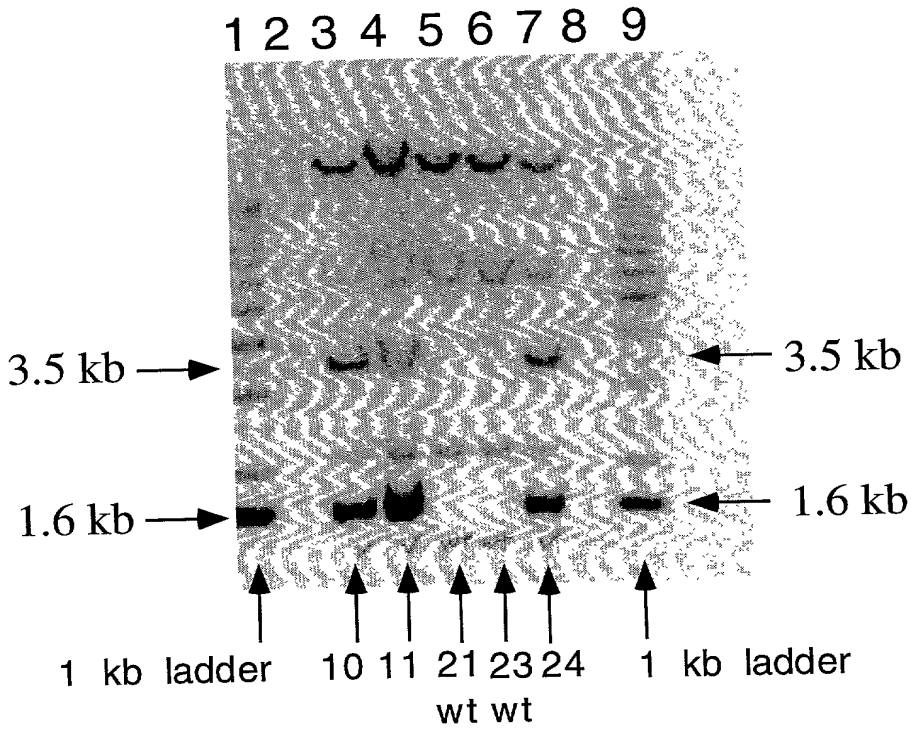

1 2 3 4 5 6 7 8 9
3.5 kb
1.6 kb
3.5 kb
1.6 kb
1 kb ladder
10 11 21 23 24
wt wt
1 kb ladder

FIG. 11

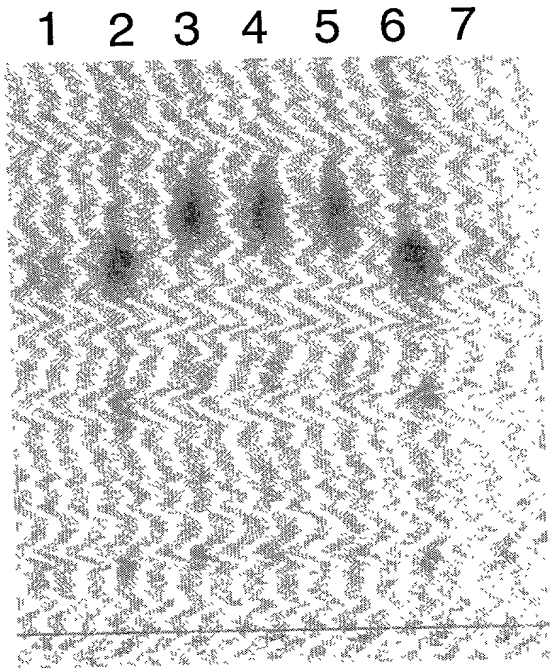


FIG. 12

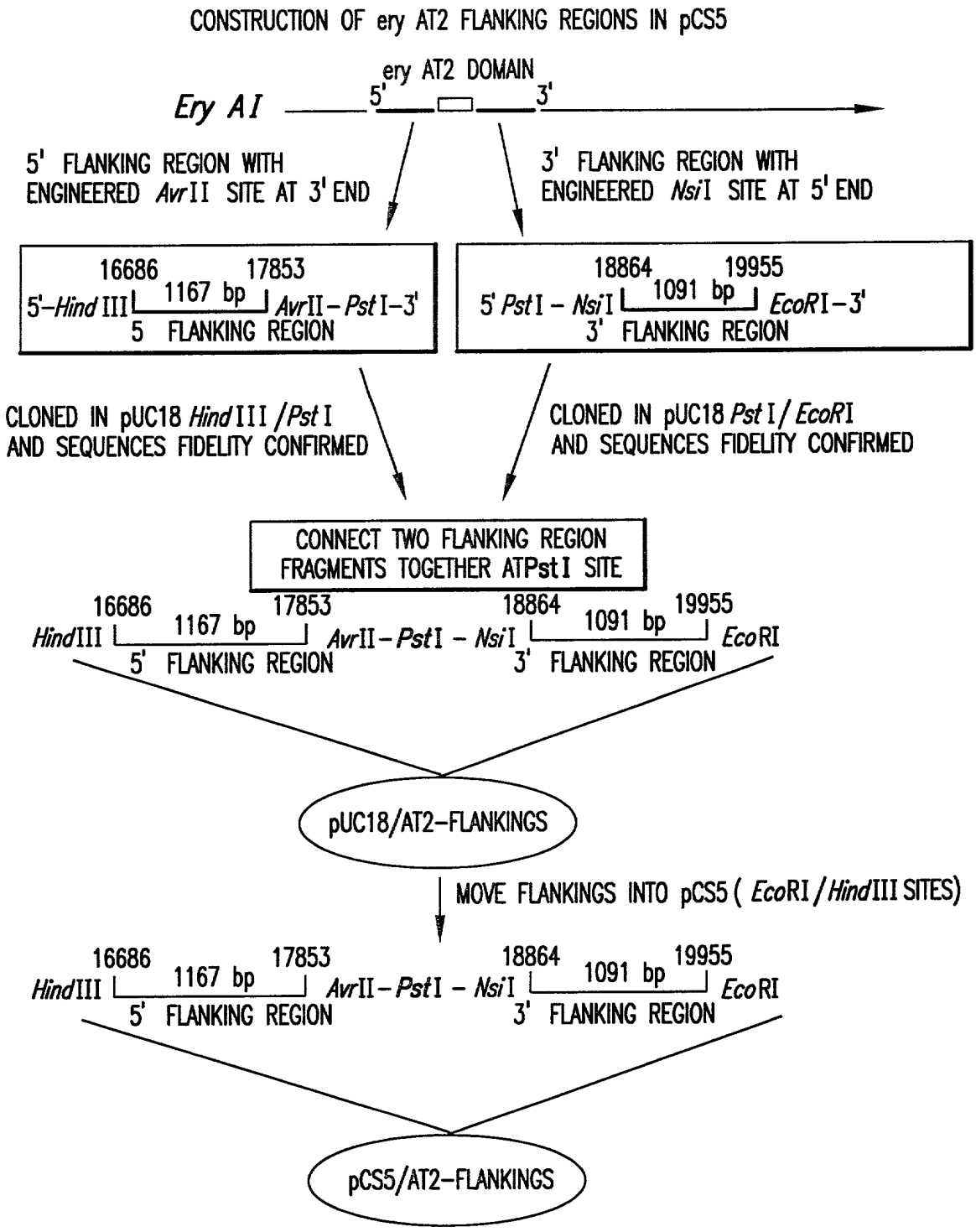

CONSTRUCTION OF ery AT2 FLANKING REGIONS IN pCS5
ery AT2 DOMAIN
Ery AI
5'
3'
5' FLANKING REGION WITH ENGINEERED AvrII SITE AT 3' END
3' FLANKING REGION WITH ENGINEERED NsiI SITE AT 5' END
16686
17853
5'-Hind III
1167 bp
AvrII-PstI-3'
5 FLANKING REGION
18864
19955
5' PstI - NsiI
1091 bp
EcoRI-3'
3' FLANKING REGION
CLONED IN pUC18 HindIII/PstI AND SEQUENCES FIDELITY CONFIRMED
CLONED IN pUC18 PstI/EcoRI AND SEQUENCES FIDELITY CONFIRMED
CONNECT TWO FLANKING REGION FRAGMENTS TOGETHER ATPstI SITE
16686
17853
18864
19955
HindIII
1167 bp
AvrII-PstI - NsiI
1091 bp
EcoRI
5' FLANKING REGION
3' FLANKING REGION
pUC18/AT2-FLANKINGS
MOVE FLANKINGS INTO pCS5 (EcoRI/HindIII SITES)
16686
17853
18864
19955
HindIII
1167 bp
AvrII-PstI - NsiI
1091 bp
EcoRI
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT2-FLANKINGS

FIG.13

SCHEME FOR CONSTRUCTION OF pEryAT2/LigAT2 INTEGRATION PLASMID

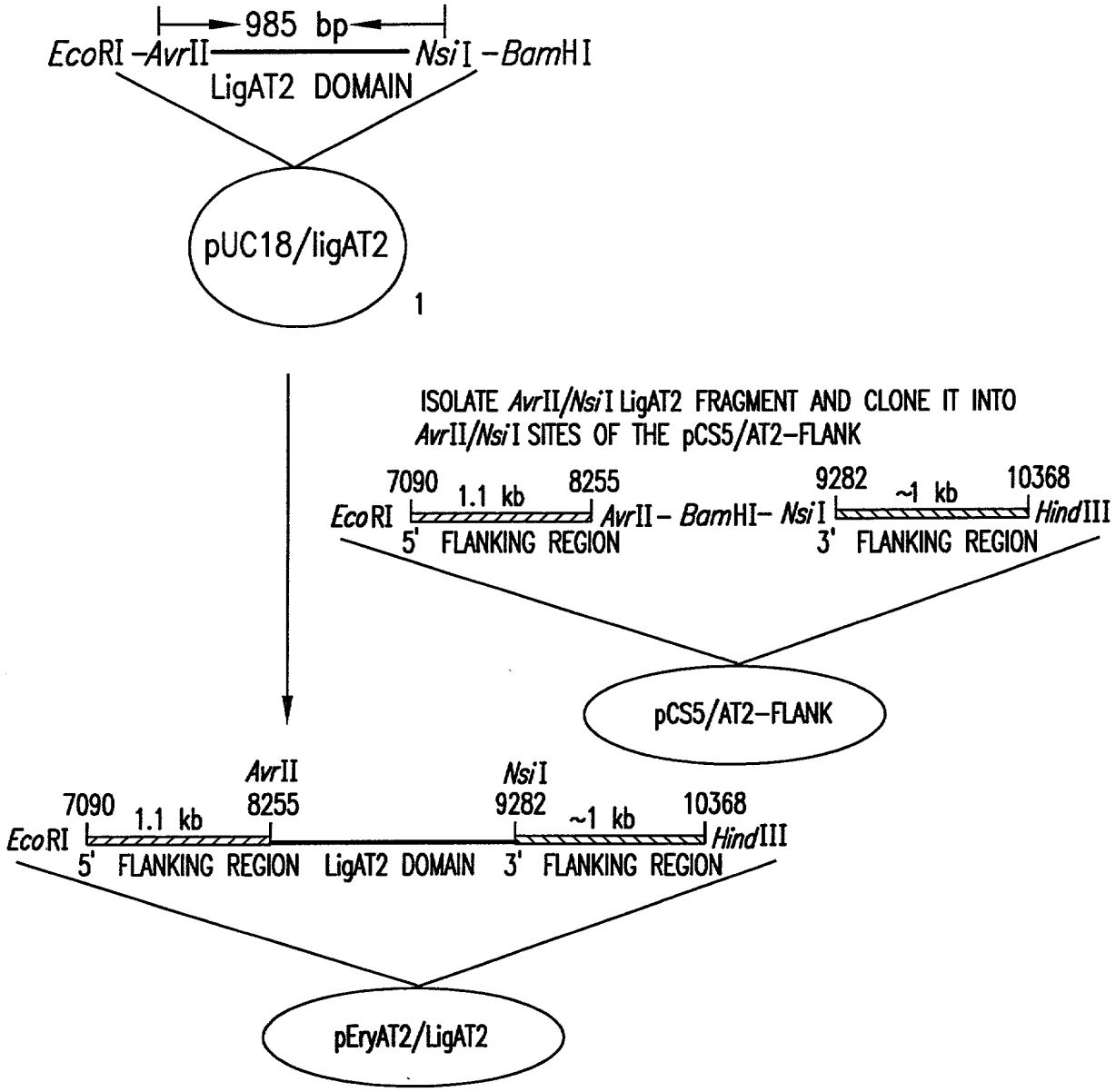


FIG.14

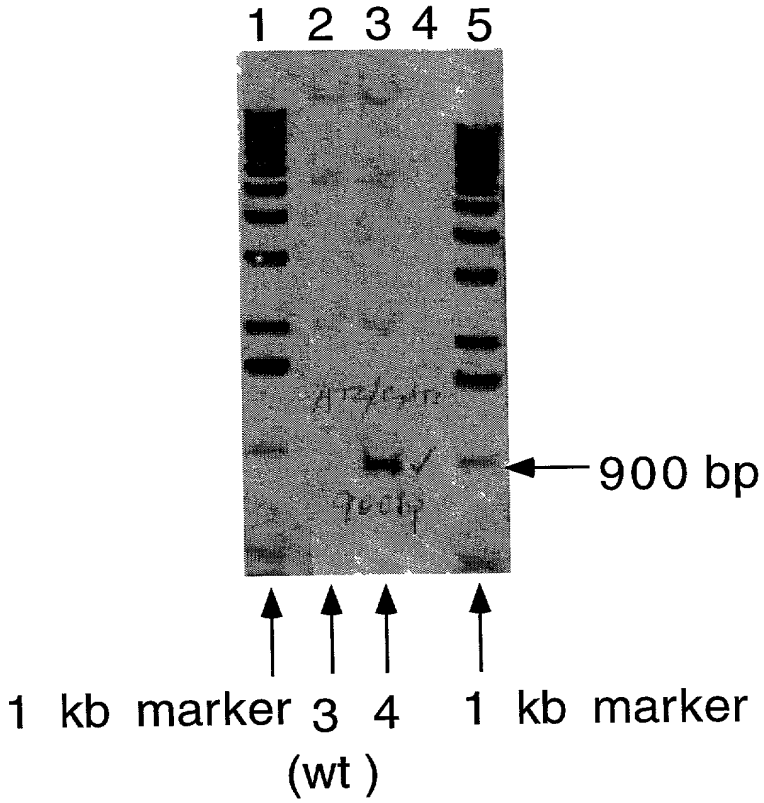


FIG. 15

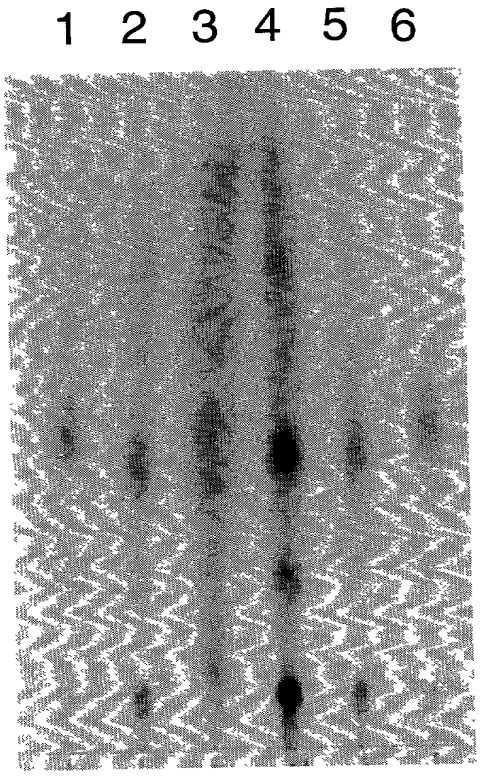


FIG.16

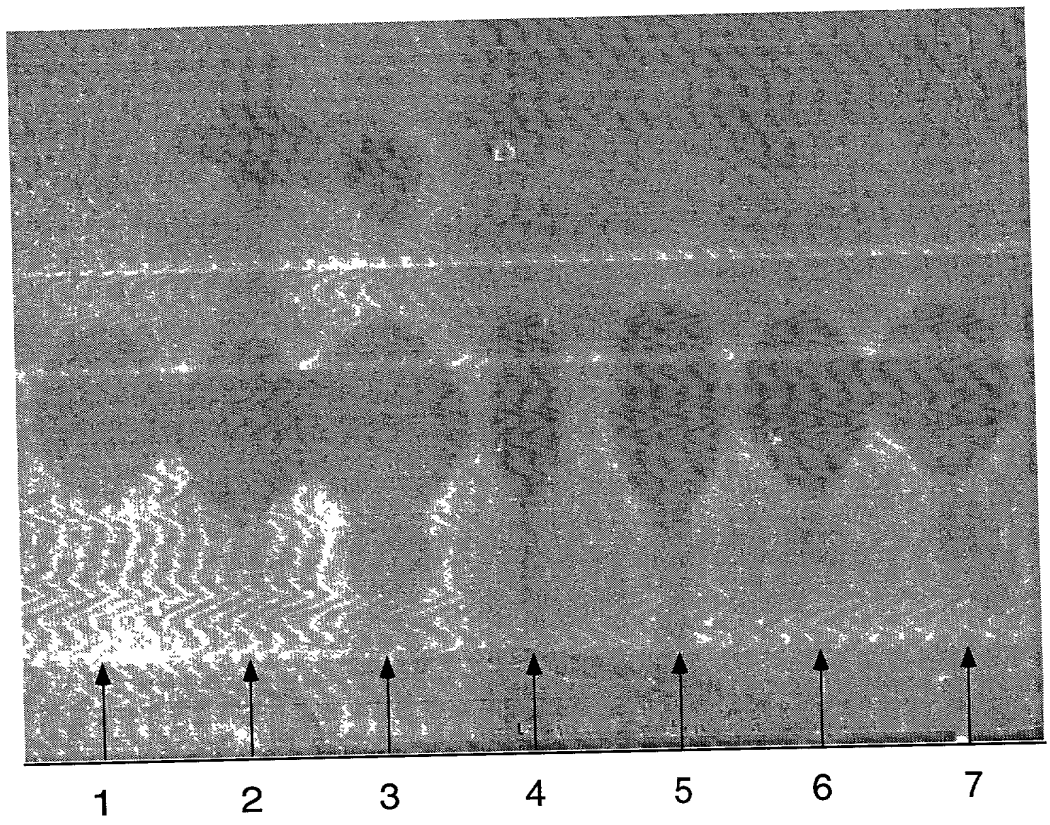
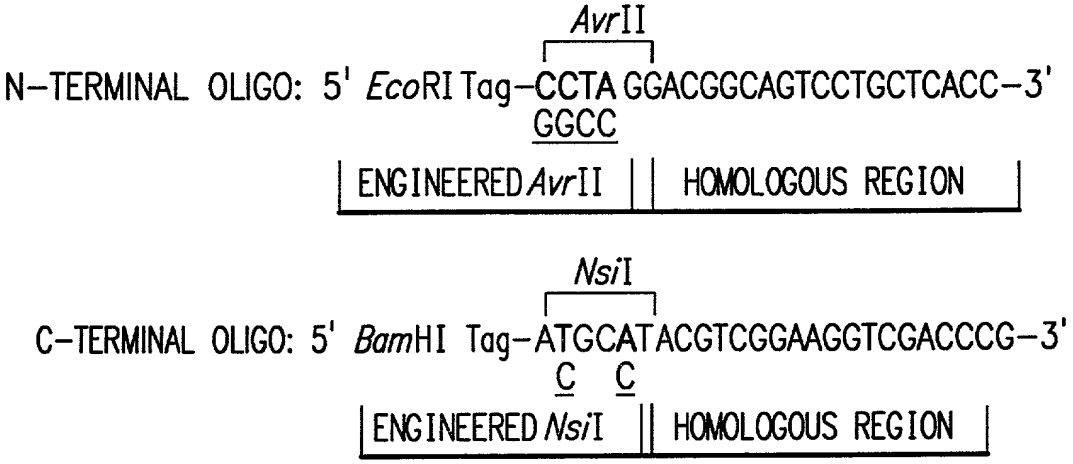


FIG. 17

```
CCTAGGACGGCAGTCCTGCTCACCGGGCAGGGTTCCCAGCGTCAGGGCATGGGGCGCGAA  60
P  R  T  A  V  L  L  T  G  Q  G  S  Q  R  Q  G  M  G  R  E   20

CTGTACGACCGGTCACCGGTGTTCGCCGCCTCGTTCGACGCGATCTGCGCTCAACTCGAC  120
L  Y  D  R  S  P  V  F  A  A  S  F  D  A  I  C  A  Q  L  D   40

GGGCAACTGCCTCGTCCCCTCAAGGACGTTCTCTTCGCCCCCGAGGGGTCGGAGGACGCC  180
G  Q  L  P  R  P  L  K  D  V  L  F  A  P  E  G  S  E  D  A   60

GCGCTCASCGACCGTACGGTGTTCACACAGGCGGCTCTGTTCGCCGTGGAGACCTCCCTG  240
A  L  I  D  R  T  V  F  T  Q  A  A  L  F  A  V  E  T  S  L   80

TTCCGGCTGTTCGAGGCCCACGGCCTCGSCCCCGACTACCTCASCGGCCACTCCATCGGC  300
F  R  L  F  E  A  H  G  L  V  P  D  Y  L  I  G  H  S  I  G   100

GAAGTGACCGCGGCCCGCCTGGCCGGGGTCCTCGATCTGGCGGACGCGTGCGTCCTGGTC  360
E  V  T  A  A  H  L  A  G  V  L  D  L  A  D  A  C  V  L  V   120

GCCCACCGCGGCCGCCTGATGCAGTCGGCCCGGGCCGGCGGCGCGATGGCCGCGGTCCAG  420
A  H  R  G  R  L  M  Q  S  A  R  A  G  G  A  M  A  A  V  Q   140

GCGAGCGAGGACGAGGTACGCGAGGCCCTCGCGACCTTCGACGATGCGGTTCCCGTGGCC  480
A  S  E  D  E  V  R  E  A  L  A  T  F  D  D  A  V  A  V  A   160

GGAGTCAACGGCCCGAACGCCACCGTCGTCTCCGGCGACGAGGACGCGGTCGAGCGGCTG  540
G  V  N  G  P  N  A  T  V  V  S  G  D  E  D  A  V  E  R  L   180

GTCGCGCGCTGGCGCGAGCAGGGCAGGCGGACGAAGCGGCTGCCGGTCAGCCACGCCTTC  600
V  A  R  W  R  E  Q  G  R  R  T  K  R  L  P  V  S  H  A  F   200

CACTCGCCGCACATGGACGGGATCGTCGACGAGTTCGTCACCGCCGTCTCCGGGCTCACC  660
H  S  P  H  M  I  G  I  V  D  E  F  V  T  A  V  S  G  L  T   220

TTCCGCTCCCCGACGLTCCCGGTCGTCTCCAACGTCACCGGGACCCTCGCCACCGTCGAC  720
F  R  S  P  T  I  P  V  V  S  N  V  T  G  T  L  A  T  V  D   240

CACCTGACCTCGCCCGCGTACTGGGCACGCCACATCCGCGAGGCCGTGCGCTTCGCCGAC  780
Q  L  T  S  P  A  Y  W  A  R  H  I  R  E  A  V  R  F  A  D   260

GGGGTGCGGTACCTGGAGGGCGAGGGCGTCACCGAATGGCTGGAGCTCGGGCCCGACGGC  840
G  V  R  Y  L  E  G  E  G  V  T  E  W  L  E  L  G  P  D  G   230

GTTCTCGTCGCCCTGGTCGAGGACTGCCTGGCGAAGGAGGCGGGATCGCTCGCGTCCGCC  900
V  L  V  A  L  V  E  D  C  L  A  K  E  A  G  S  L  A  S  A   300

CTGCGCAAGGGGGCGAGCGAGCCCCACACCGTGGGCGCGGCCATGGCCCGCGCGGTGCTG  960
L  R  K  G  A  S  E  P  H  T  V  G  A  A  M  A  R  A  V  L   320

CGCGGATCCGGCCCCGACTGGGCGGCGGTGTTCCCCGGCGCACGGCGGGTCGACCTTCCG  1020
R  G  S  G  P  D  W  A  A  V  F  P  G  A  R  R  V  D  L  P   340

ACGTATGCAT                                                    1030
T  Y  A                                                        343
```

FIG. 18

PCR OLIGOS:



PCR CLONING:

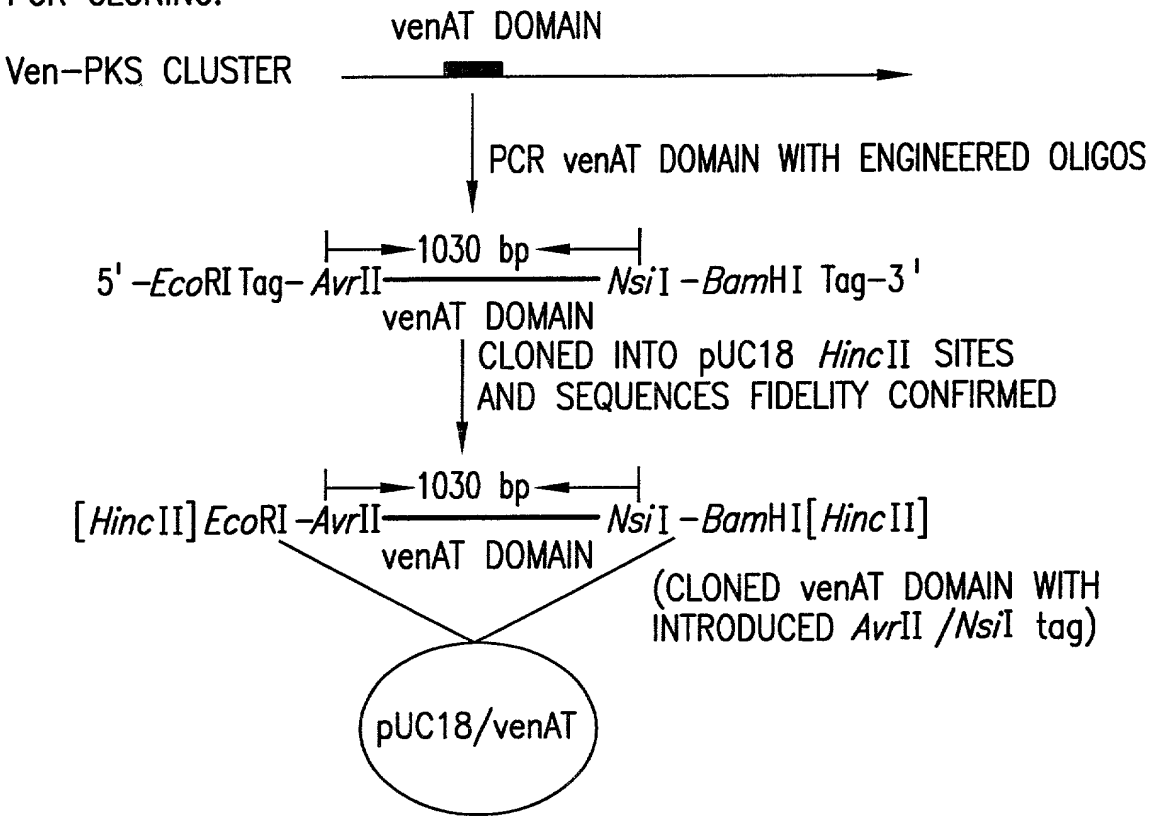


FIG.19

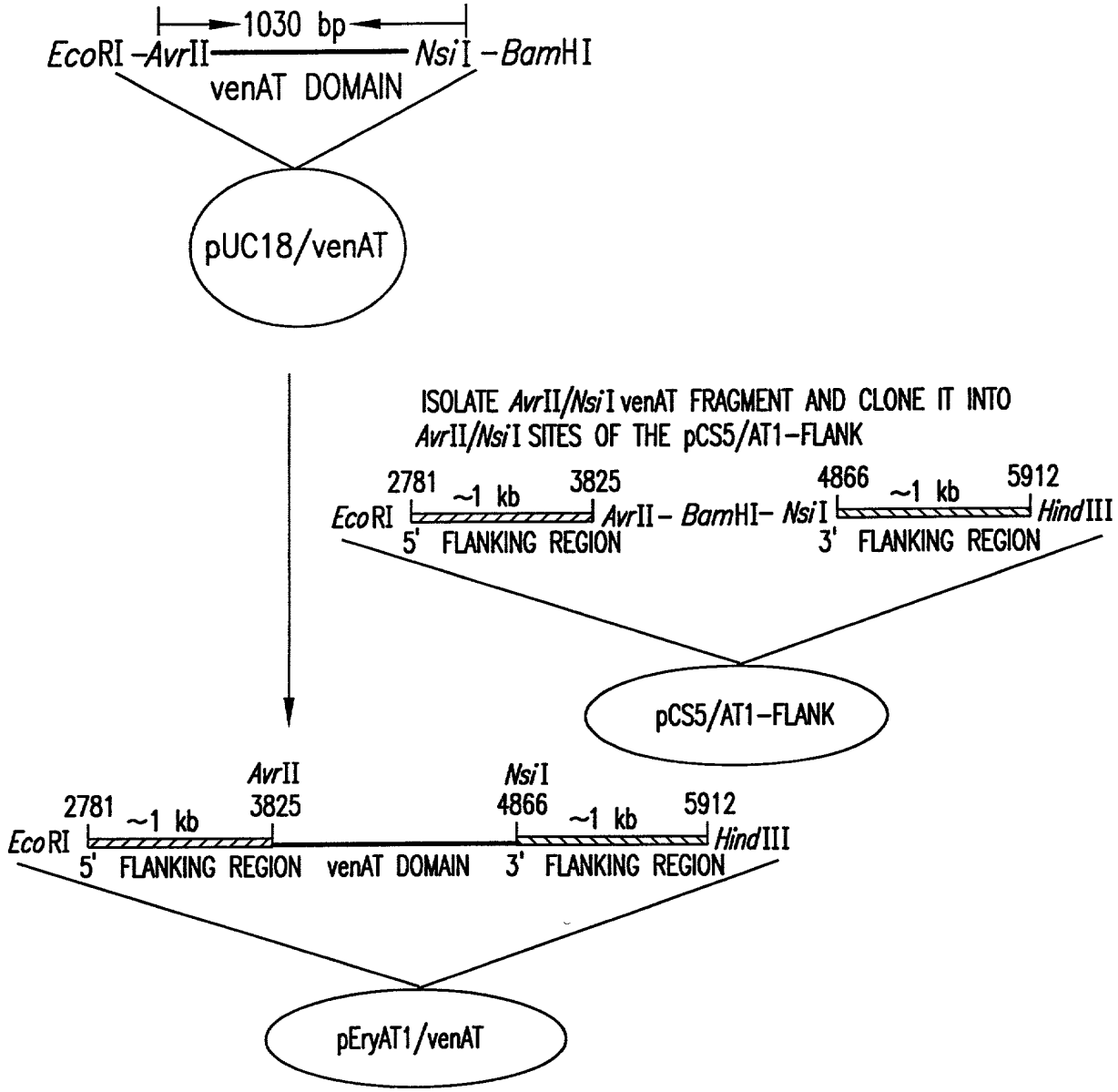

1030 bp
EcoRI -AvrII- NsiI -BamHI
venAT DOMAIN
pUC18/venAT
ISOLATE AvrII/NsiI venAT FRAGMENT AND CLONE IT INTO
AvrII/NsiI SITES OF THE pCS5/AT1-FLANK
2781
~1 kb
3825
EcoRI
AvrII- BamHI- NsiI
4866
~1 kb
5912
HindIII
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT1-FLANK
AvrII
NsiI
2781
~1 kb
3825
4866
~1 kb
5912
EcoRI
HindIII
5' FLANKING REGION
venAT DOMAIN
3' FLANKING REGION
pEryAT1/venAT

FIG.20

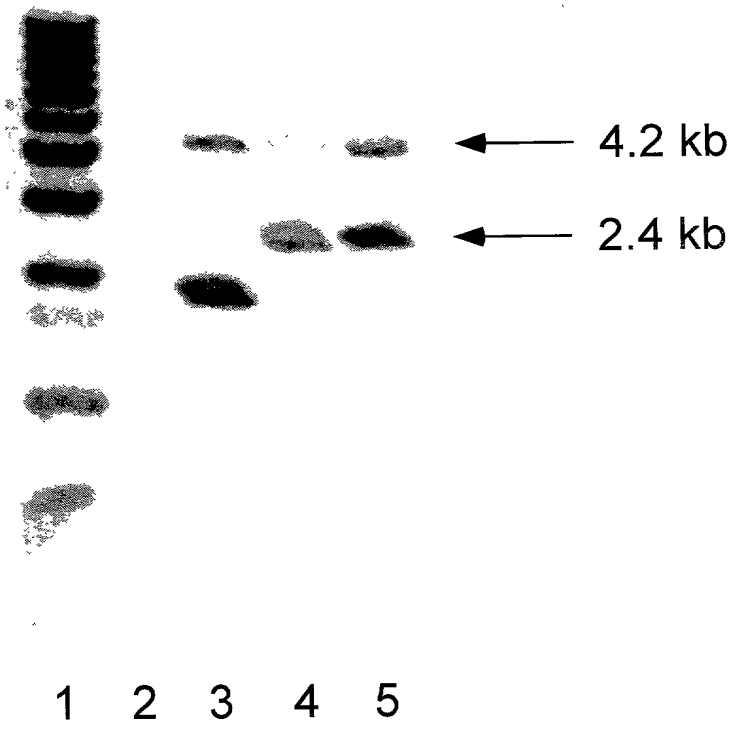


FIG. 21

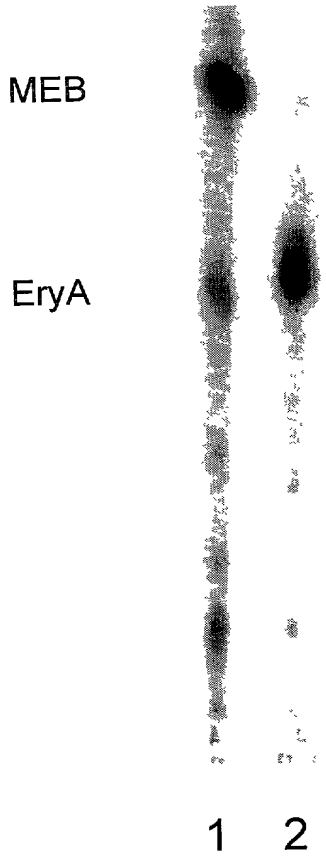
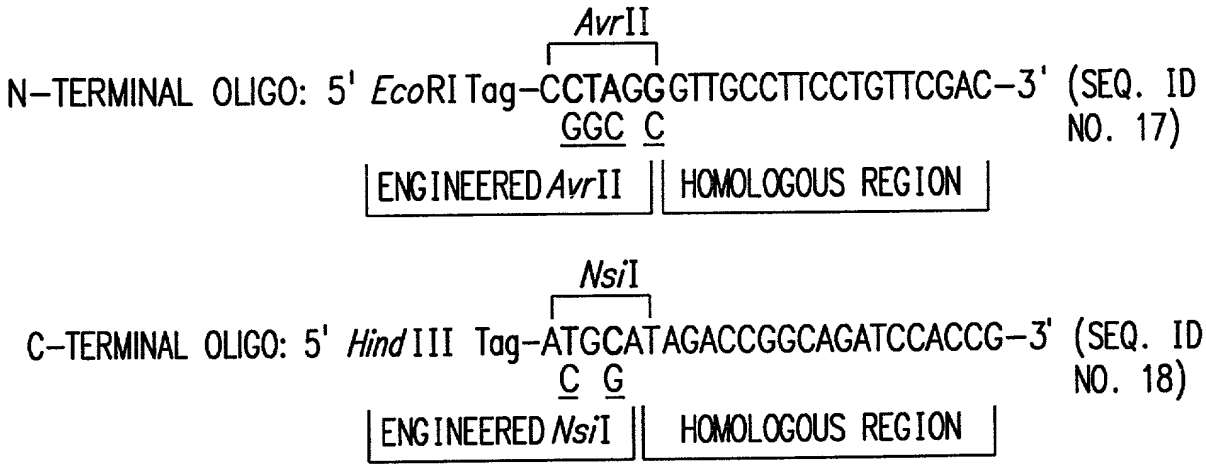


FIG. 22

PCR OLIGOS:



PCR CLONING:

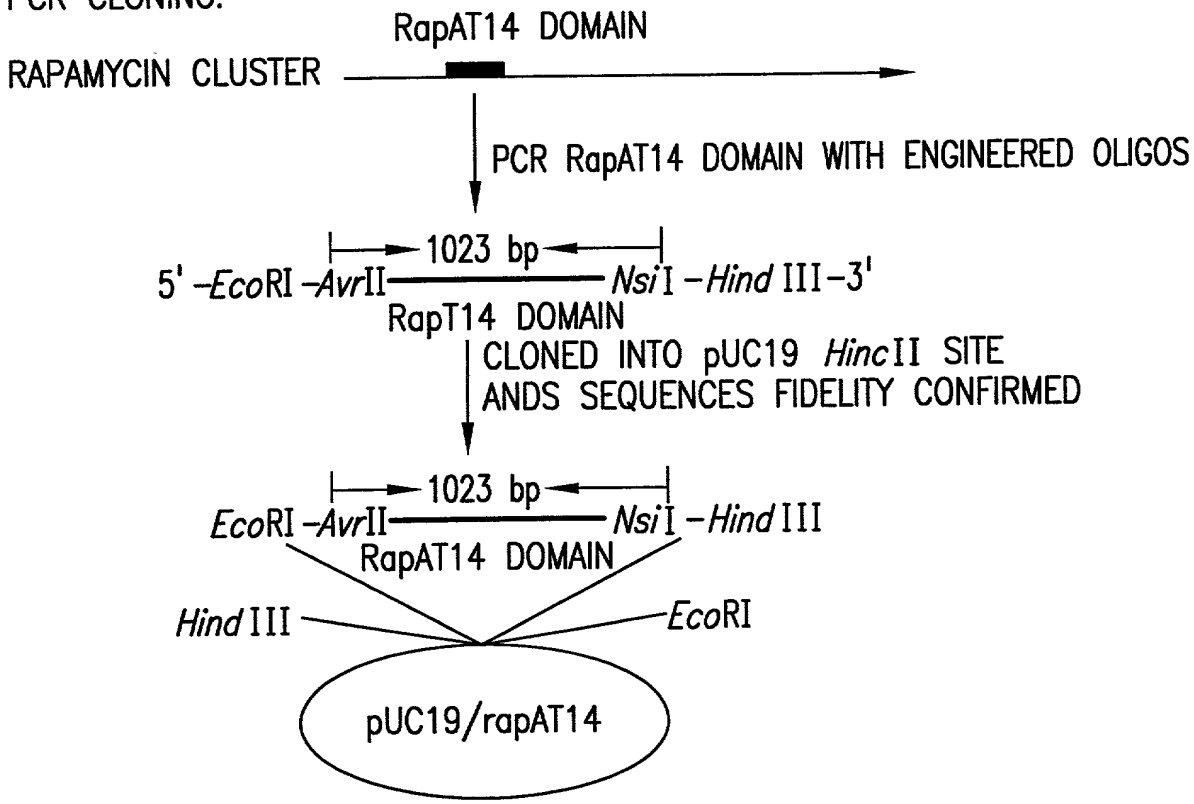


FIG.23

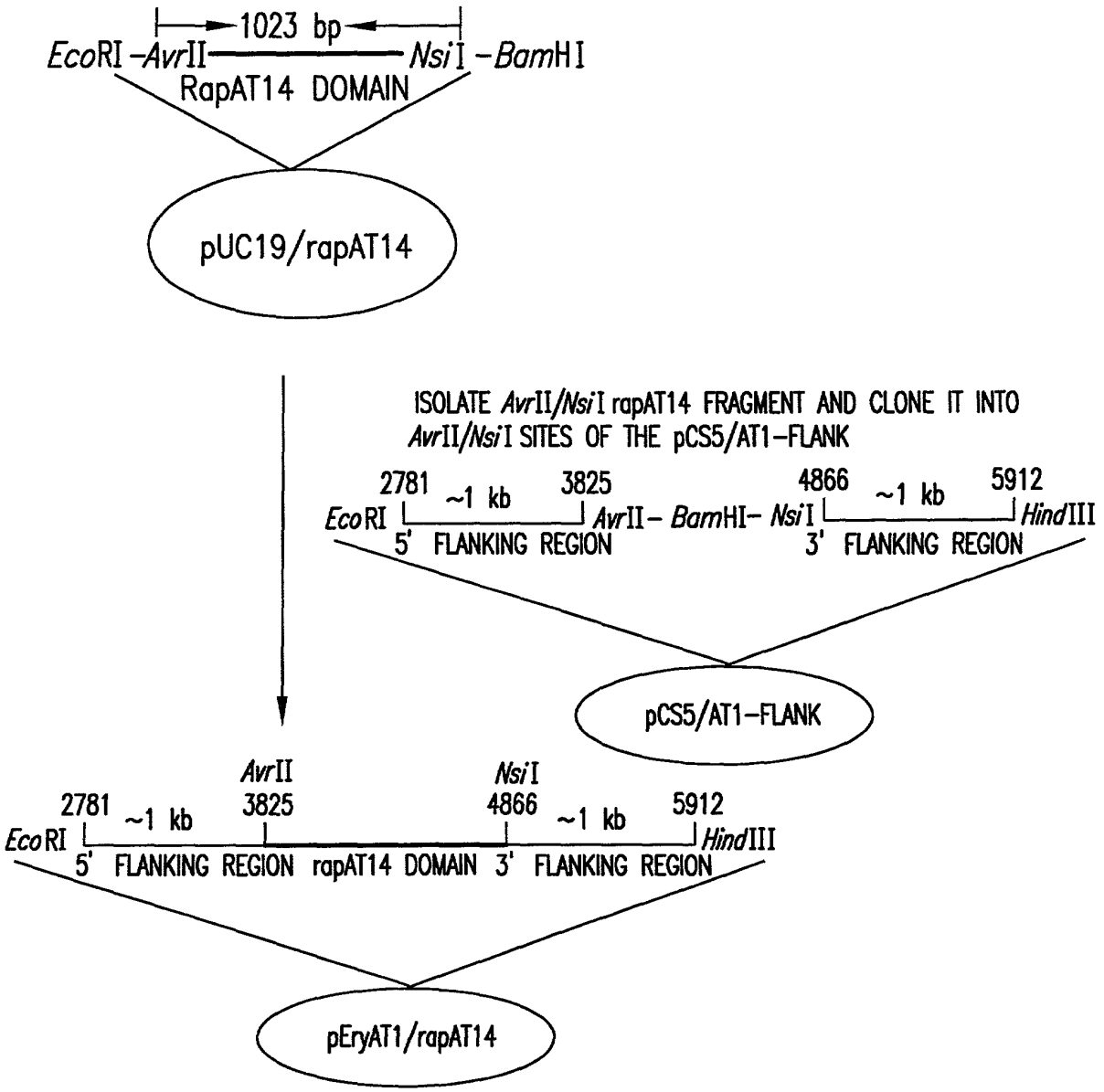

1023 bp
EcoRI -AvrII- NsiI -BamHI
RapAT14 DOMAIN
pUC19/rapAT14
ISOLATE AvrII/NsiI rapAT14 FRAGMENT AND CLONE IT INTO
AvrII/NsiI SITES OF THE pCS5/AT1-FLANK
2781
~1 kb
3825
4866
~1 kb
5912
EcoRI
AvrII- BamHI- NsiI
HindIII
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT1-FLANK
AvrII
NsiI
2781
~1 kb
3825
4866
~1 kb
5912
EcoRI
HindIII
5' FLANKING REGION rapAT14 DOMAIN 3' FLANKING REGION
pEryAT1/rapAT14

FIG.24

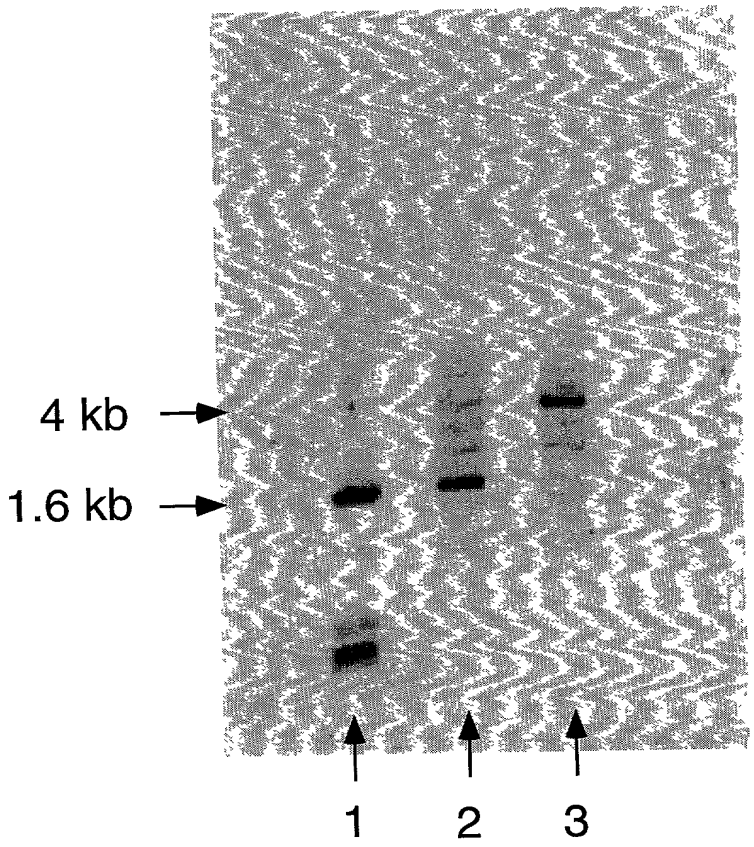


FIG. 25

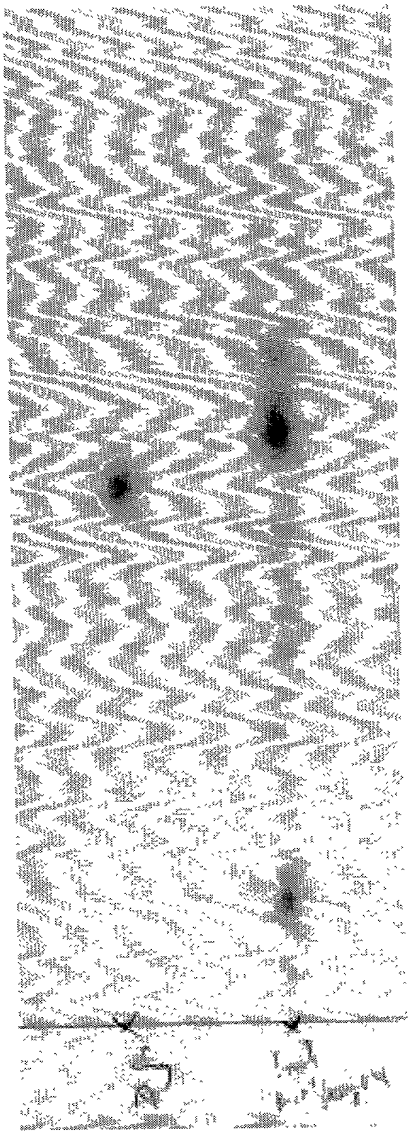


FIG. 26

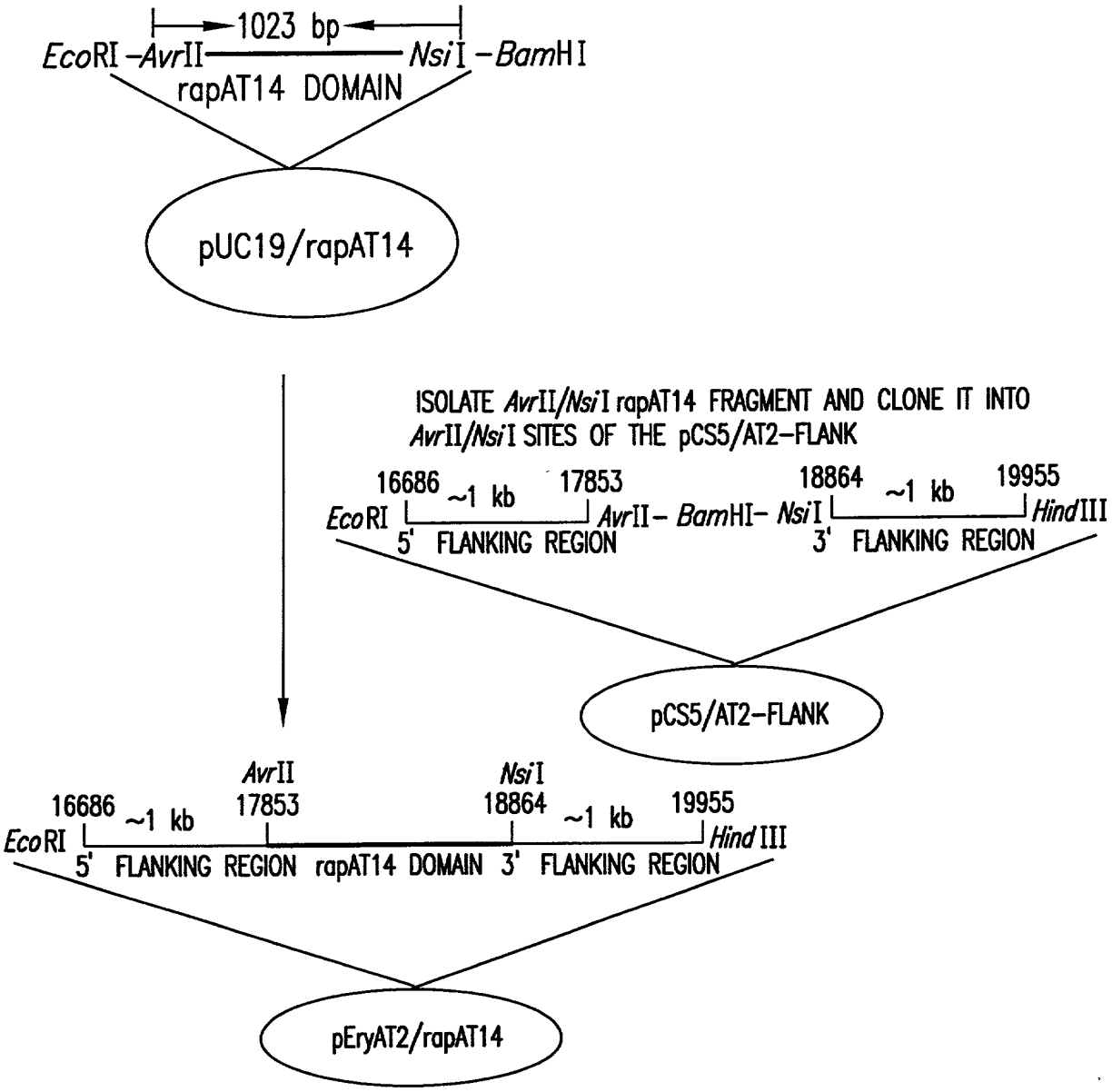

1023 bp
EcoRI -AvrII- NsiI -BamHI
rapAT14 DOMAIN
pUC19/rapAT14
ISOLATE AvrII/NsiI rapAT14 FRAGMENT AND CLONE IT INTO
AvrII/NsiI SITES OF THE pCS5/AT2-FLANK
16686
~1 kb
17853
EcoRI
AvrII- BamHI- NsiI
18864
~1 kb
19955
HindIII
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT2-FLANK
AvrII
NsiI
16686
~1 kb
17853
18864
~1 kb
19955
EcoRI
HindIII
5' FLANKING REGION rapAT14 DOMAIN 3' FLANKING REGION
pEryAT2/rapAT14

FIG.27

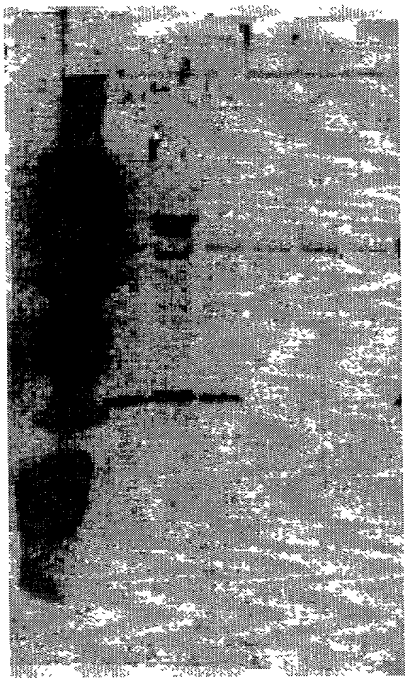


FIG. 28

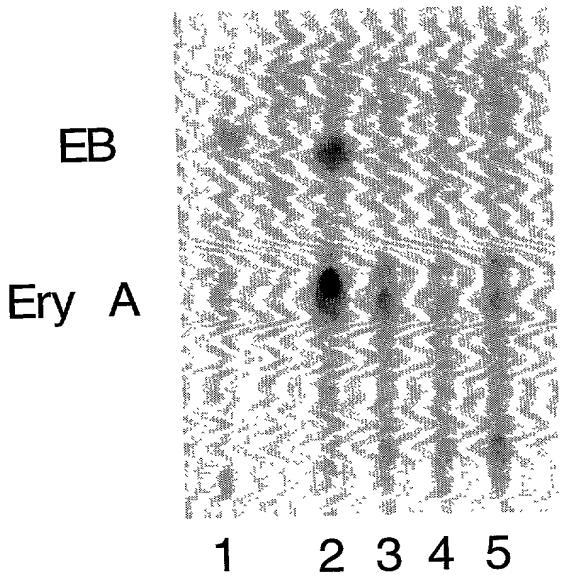


FIG. 29

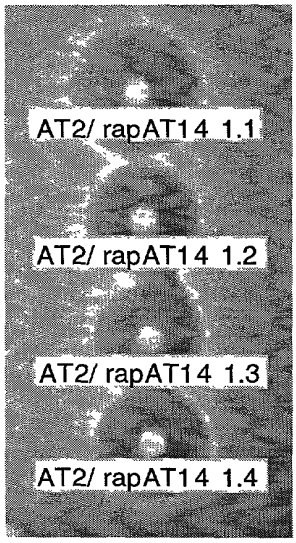


FIG. 30

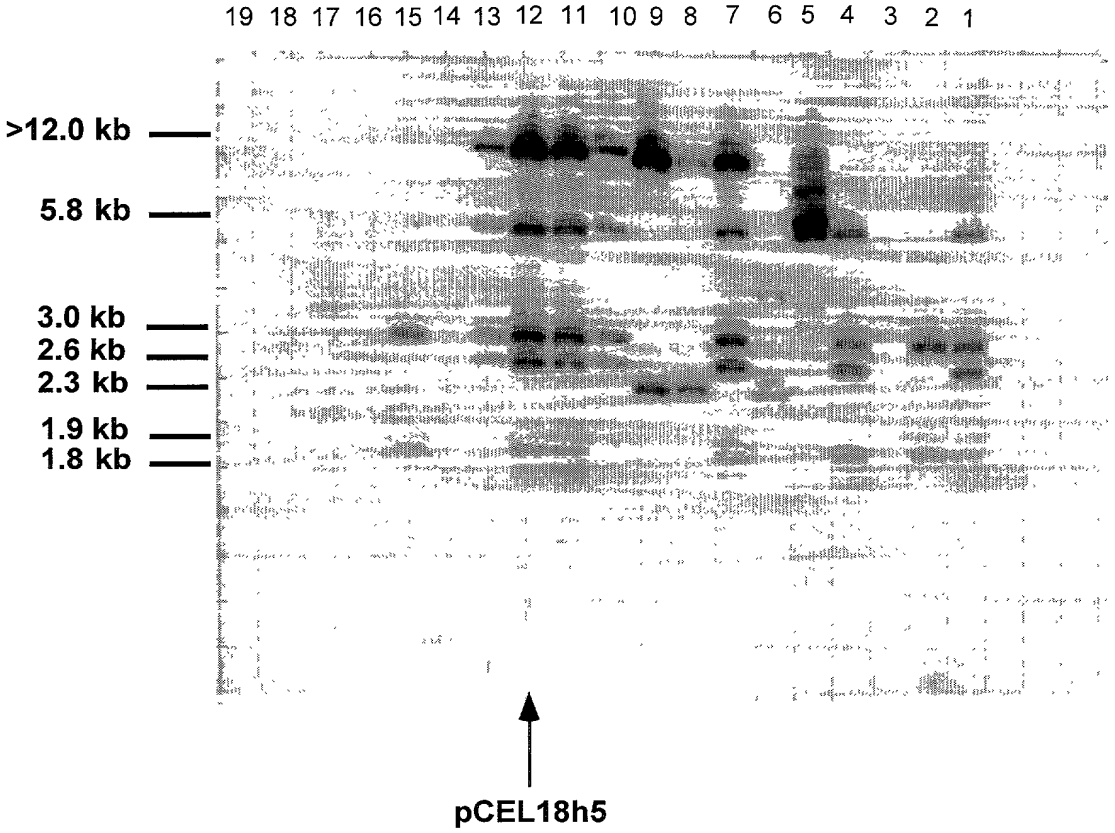

19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1
>12.0 kb
5.8 kb
3.0 kb
2.6 kb
2.3 kb
1.9 kb
1.8 kb
pCEL18h5

FIG. 31

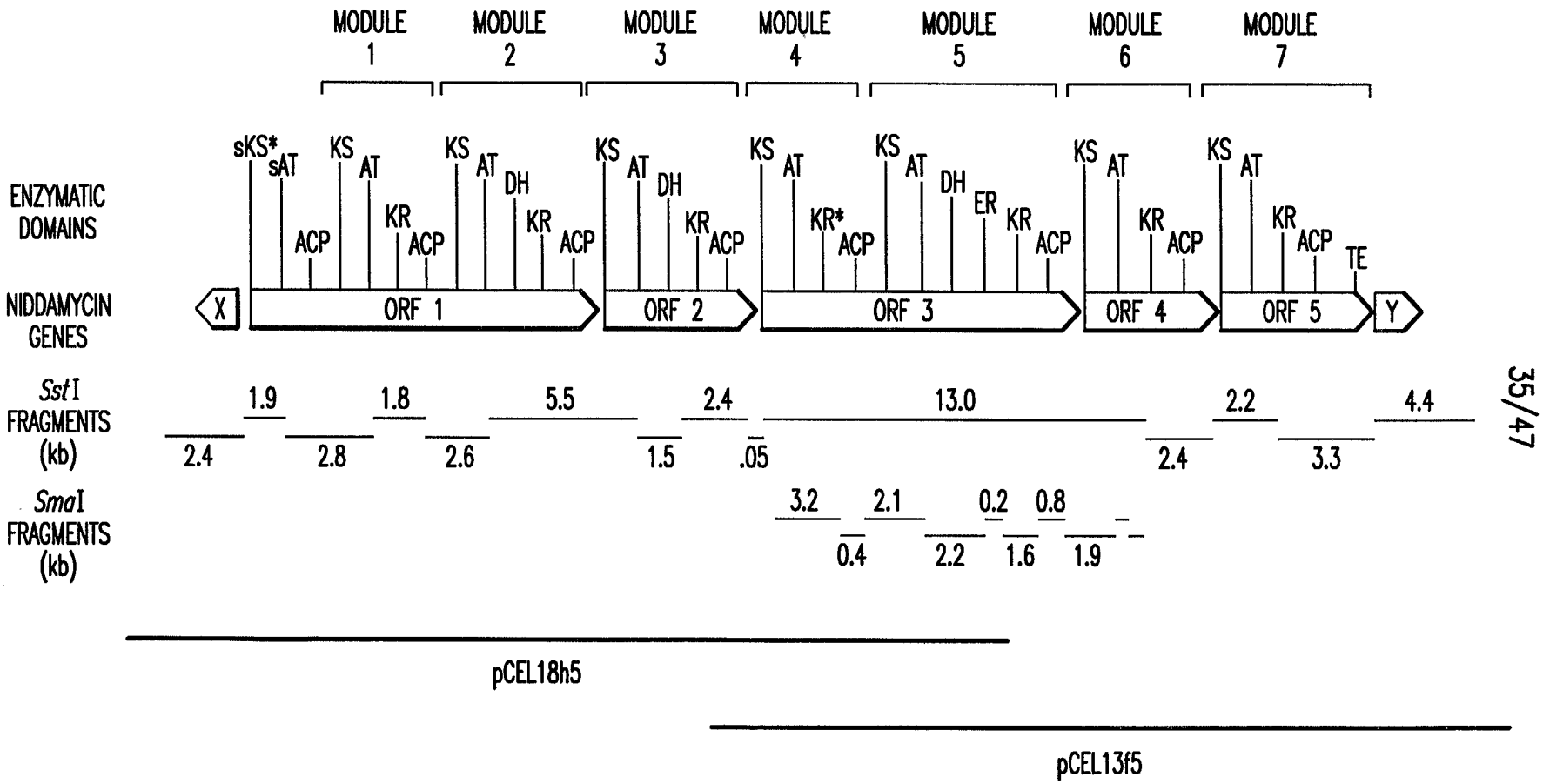

MODULE 1
MODULE 2
MODULE 3
MODULE 4
MODULE 5
MODULE 6
MODULE 7
ENZYMATIC DOMAINS
NIDDAMYCIN GENES
X
ORF 1
ORF 2
ORF 3
ORF 4
ORF 5
Y
sKS*
sAT
KS
AT
ACP
KR
DH
KR*
ER
TE
SstI FRAGMENTS (kb)
1.9
1.8
5.5
2.4
13.0
2.2
4.4
2.4
2.8
2.6
1.5
.05
2.4
3.3
SmaI FRAGMENTS (kb)
3.2
2.1
0.2
0.8
0.4
2.2
1.6
1.9
pCEL18h5
pCEL13f5

FIG.32

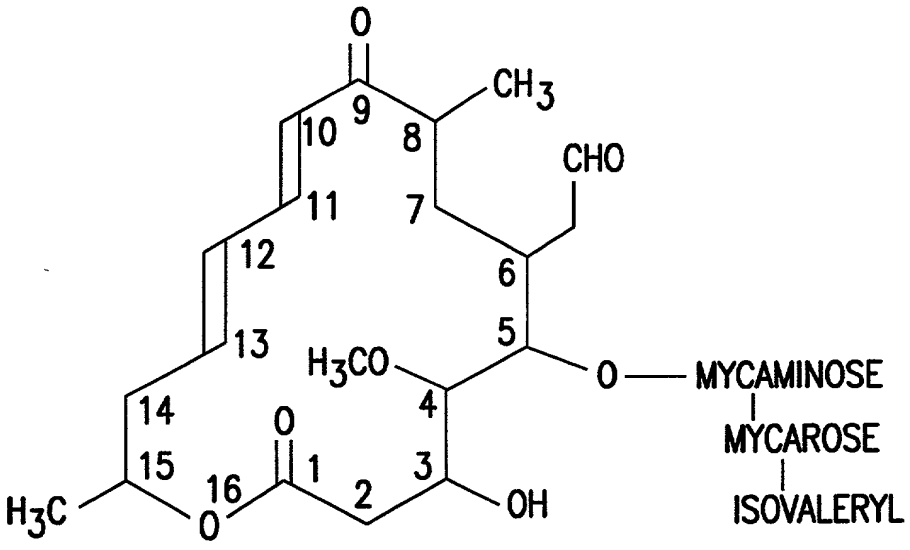

O
CH3
9
10
8
CHO
11
7
12
6
5
13
H3CO
O
MYCAMINOSE
14
4
MYCAROSE
O
15
1
3
16
2
H3C
O
OH
ISOVALERYL

FIG.33

GCCGACCGTGTCGTGTTCGTGTTCCCCGGCCAGGGCTCGCAGTGGGCCGGAATGGCCGAG 60
A D R V V F V F P G Q G S Q W A G M A E 20

GGCTGCTGGAGCGGTCCGGCGCGTTCCGGAGTGCGGCCGACTCGTGCGACGCCGCGCTG 120
G L L E R S G A F R S A A D S C D A A L 40

CGGCCGTACCTCGGCTGCTCGGTGCTGAGCGTGCTGCGCGGGGAACCGGACGCGCCCTCG 180
R P Y L G W S V L S V L R G E P D A P S 60

CTCGACCGGGTCGACGTCGTGCAGCCGGTGCTGTTCACGATGATGGTCTCGCTCGCGGCG 240
L D R V D V V Q P V L F T M M V S L A A 80

GTCTGGCGTGCGCTGGGCGTGGAACCGGCGGCGGTCGTCGGGCACTCGCAGGGTGAGATC 300
V W R A L G V E P A A V V G H S Q G E I 100

GCCGCTGCCCATGTCGCCGGTGCGCTGTCGCTGGACGACTCGGCCCGGATCGTCGCCCTG 360
A A A H V A G A L S L D D S A R I V A L 120

CGCAGTCGGGCGTGGCTCGGACTGGCGGGCAAGGGCGGCATGGTGGCGGTGCCGATGCCG 420
R S R A W L G L A G K G G M V A V P M P 140

GCGGAGGAGCTGCGGCCGCGGCTGGTGACGTGGGGGGACCGTCTGGCCGTCGCCGCCGTC 480
A E E L R P R L V T W G D R L A V A A V 160

AACAGCCCCGGTTCCTGCGCCGTCGCAGGCGACCCGGAGGCGCTGGCCGAACTGGTGGCG 540
N S P G S C A V A G D P E A L A E L V A 180

CTGCTGACCGGTGAGGGGGTGCACGCCCGGCCGATCCCCGGCGTCGACACGGCGGGCCAC 600
L L T G E G V H A R P I P G V D T A G H 200

TCGCCGCAGGTGGACGCGTTGCGGGCTCATCTGCTGGAGGTGCTGGCCCCGGTCGCCCCC 660
S P Q V D A L R A H L L E V L A P V A P 220

CGACCGGCCGACATCCCGTTCTACTCGACGGTGACCGGCGGGCTGCTGGACGGCACCGAG 720
R P A D T P F Y S T V T G G L L D G T E 240

CTGGACGCGACGTACTGGTACCGCAACATGCGCGAGCCCGTCGAGTTCGAGCGGGCCACA 780
L D A T Y W Y R N M R E P V E F E R A T 260

CGGGCGCTGATCGCCGACGGCCACGACGTCTTCCTGGAGACGAGCCCGCATCCCATGCTG 840
R A L I A D G H D V F L E T S P H P M L 280

GCCGTGGCGCTGGAGCAGACGGTCACCGACGCCGGCACCGACGCGGCGGTGCTCGGGACC 900
A V A L E Q T V T D A G T D A A V L G T 300

CTGCGCCGCCGCCACGGCGGTCCTCGCGCGCTGGCCCTGGCCGTCTGCCGCGCCTTCGCG 960
L R R R H G G P R A L A L A V C R A F A 320

CACGGCGTGGAGGTGGACCCCGAGGCGGTCTTCGGTCCGGGCGCACGGCCCGTGGAGTTG 1020
H G V E V D P E A V F G P G A R P V E L 340

CCCACCTATCCG 1032
P T Y P 344

FIG. 34

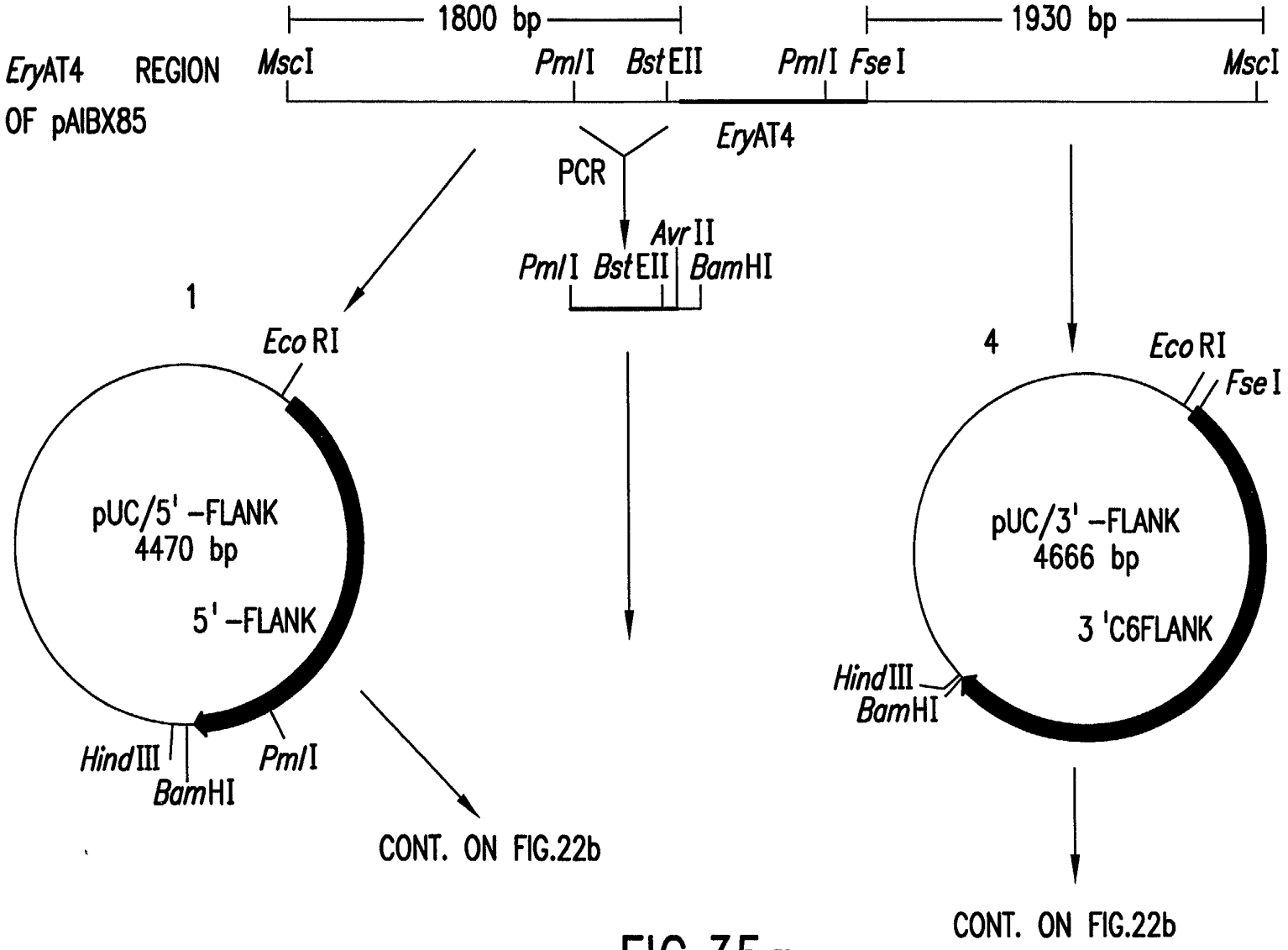

1800 bp
1930 bp
EryAT4 REGION OF pAIBX85
MscI
PmlI
BstEII
PmlI
FseI
MscI
EryAT4
PCR
AvrII
PmlI BstEII BamHI
1
EcoRI
pUC/5'-FLANK
4470 bp
5'-FLANK
HindIII
BamHI
PmlI
CONT. ON FIG.22b
4
EcoRI
FseI
pUC/3'-FLANK
4666 bp
3'C6FLANK
HindIII
BamHI
CONT. ON FIG.22b

FIG.35a

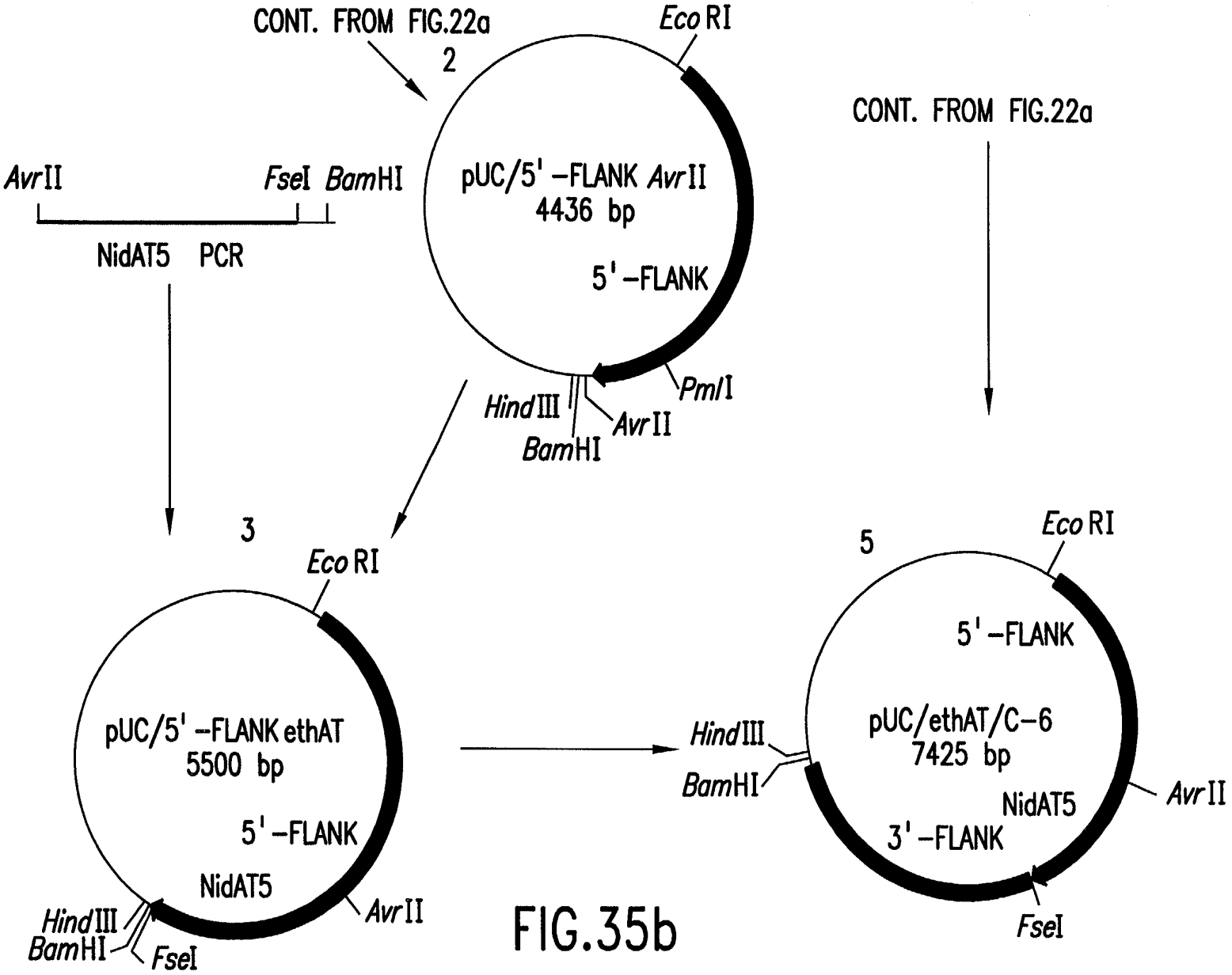
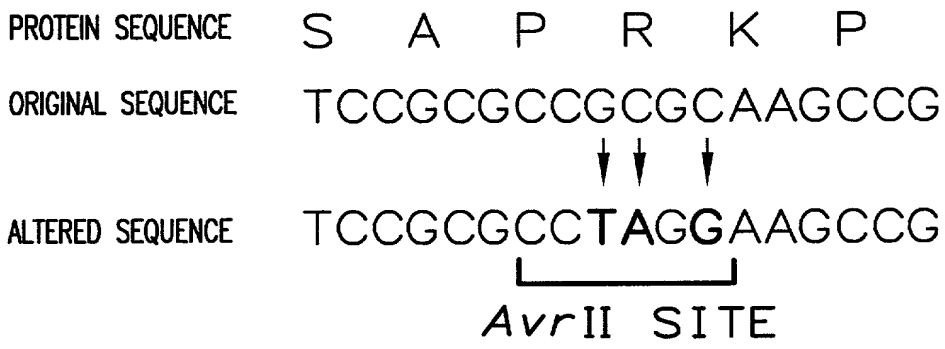
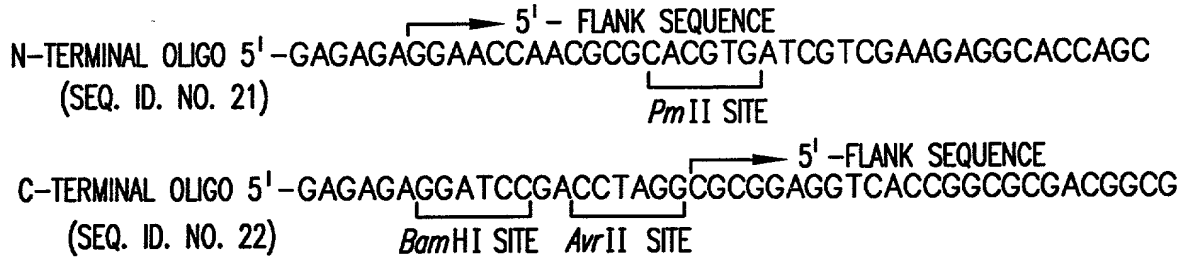

CONT. FROM FIG.22a
2
Eco RI
pUC/5'-FLANK AvrII
4436 bp
5'-FLANK
AvrII
FseI
BamHI
NidAT5 PCR
PmlI
HindIII
AvrII
BamHI
CONT. FROM FIG.22a
3
Eco RI
pUC/5'-FLANK ethAT
5500 bp
5'-FLANK
NidAT5
AvrII
HindIII
BamHI
FseI
5
Eco RI
5'-FLANK
pUC/ethAT/C-6
7425 bp
NidAT5
3'-FLANK
AvrII
HindIII
BamHI
FseI

FIG.35b



PCR OLIGOS FOR 5'-FLANK *Avr*II SITE



PCR OLIGOS FOR NidAT5 FRAGMENT

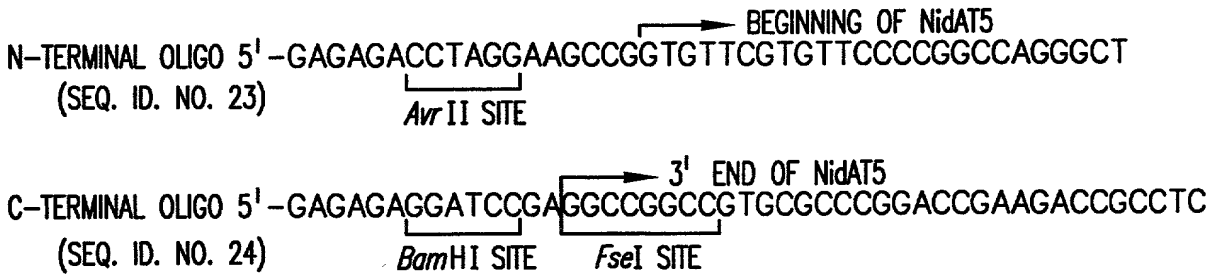


FIG.36

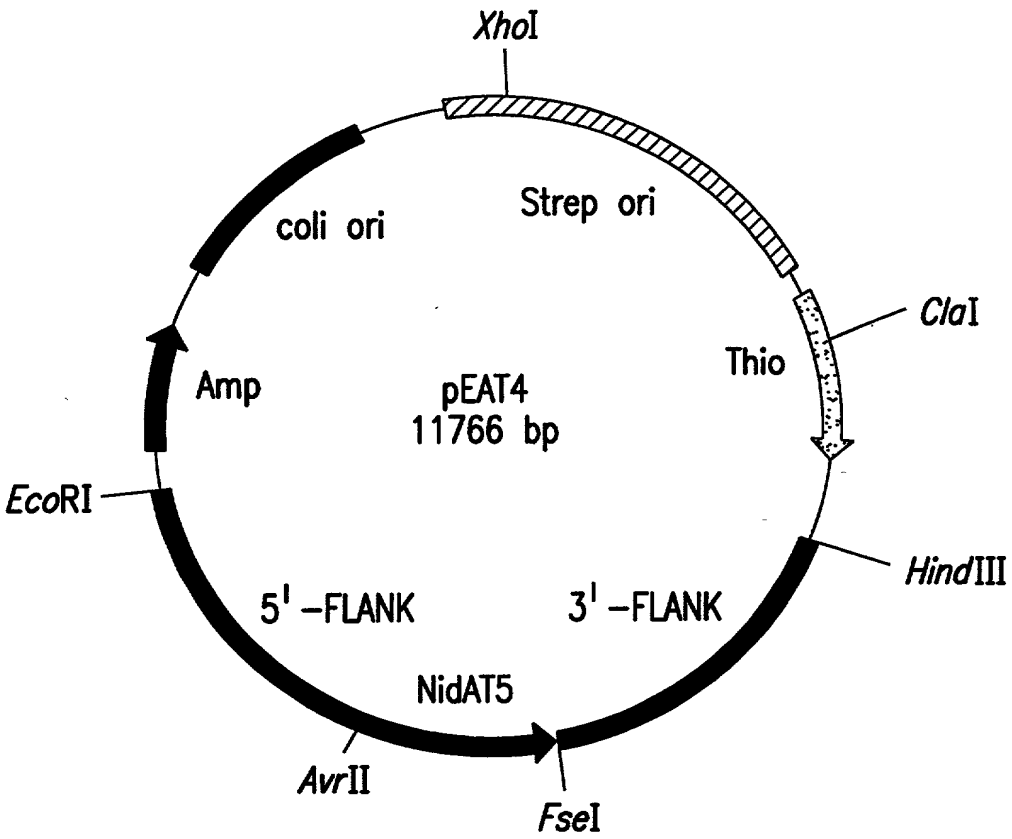

XhoI
Strep ori
coli ori
ClaI
Thio
Amp
pEAT4
11766 bp
EcoRI
HindIII
5' -FLANK
3' -FLANK
NidAT5
AvrII
FseI

FIG.37

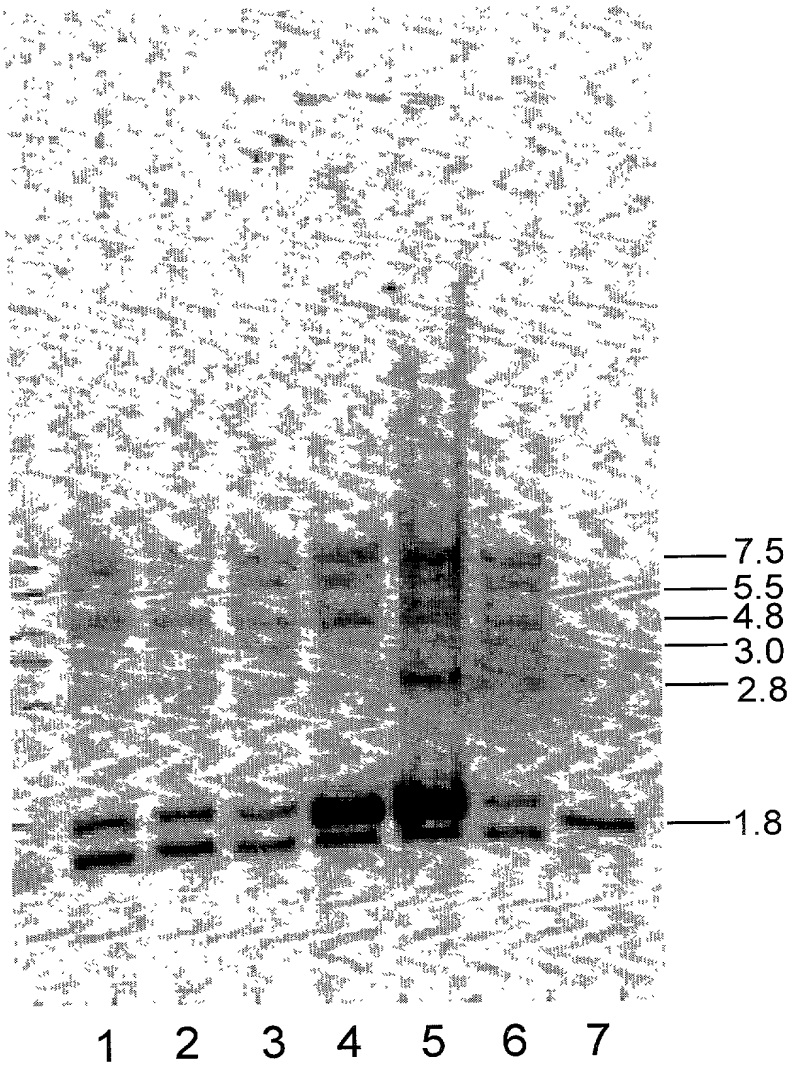
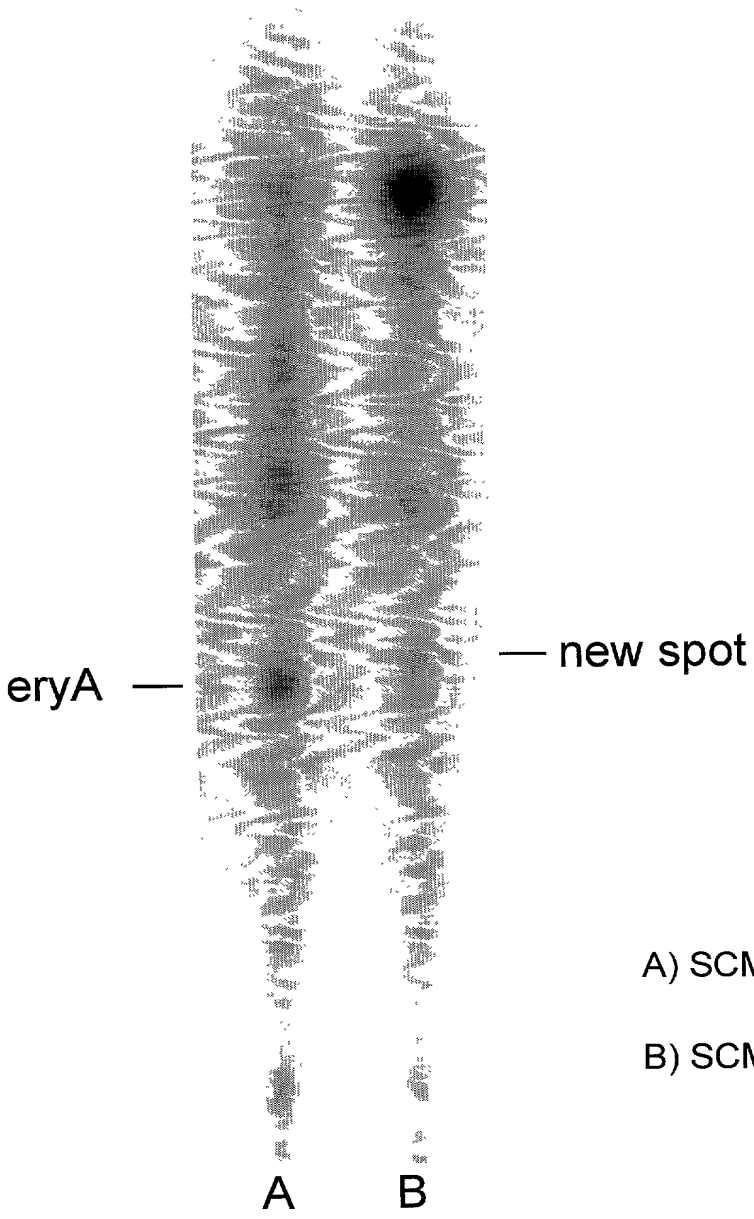


FIG. 38



A) SCM only

B) SCM + 50mM butyric acid

FIG. 39

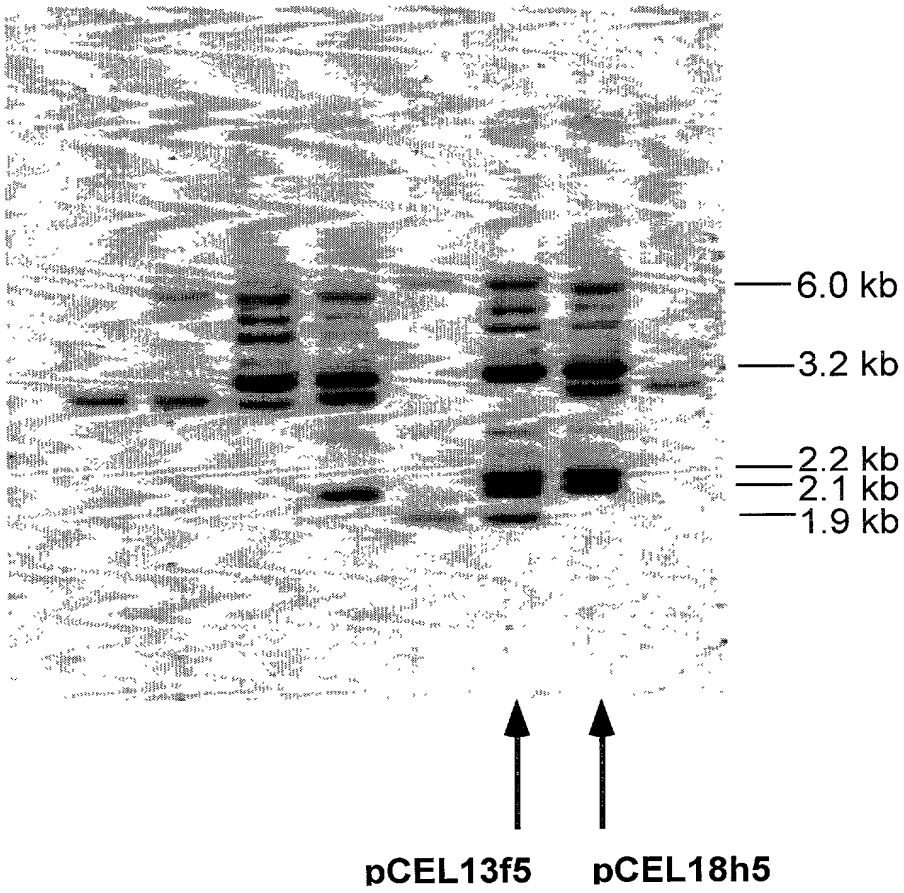
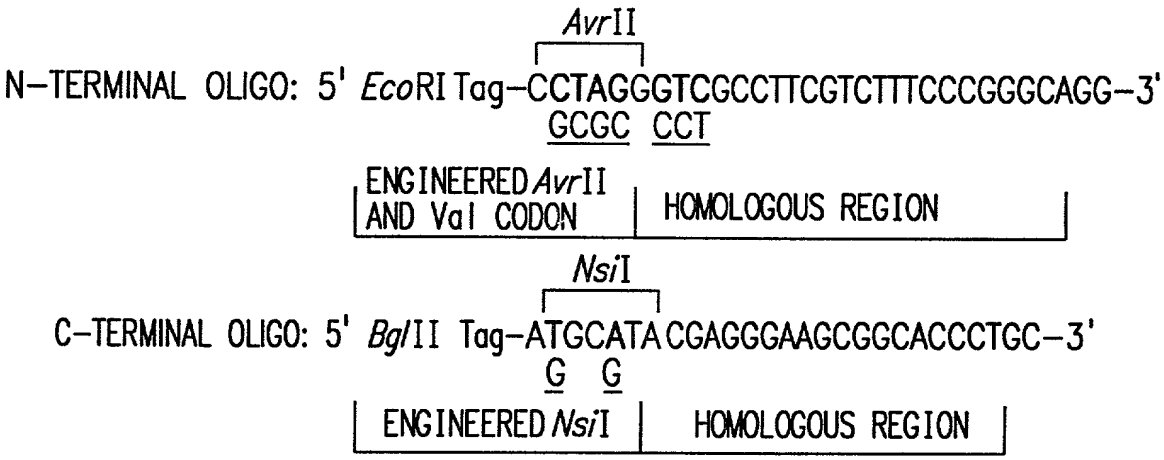


FIG. 40

```
CGCGCGCCTGCCTTCGTCTTTCCCGGGCAGGGCGCCCAGTGGGCCGGACTGGGAGCGCGG 60
R  A  P  A  F  V  F  P  G  Q  G  A  Q  W  A  G  L  G  A  R  20
CTCCTCGCGGACTCCCCCGTCTTCCGCGCCAGGGCCGAGGCATGCGCGCGGGCGCTGGAG 120
L  L  A  D  S  P  V  F  R  A  R  A  E  A  C  A  R  A  L  E  40
CCTCACCTCGACTGGTCGGTCCTCGACGTGCTGGCCGGCGCCCCGGGCACCCCTCCCATC 180
P  H  L  D  W  S  V  L  D  V  L  A  G  A  P  G  T  P  P  I  60
GACCGGGCCGACGTGGTGCAGCCGGTGCTGTTCACCACGATGGTCTCGCTGGCCGCCCTC 240
D  R  A  D  V  V  Q  P  V  L  F  T  T  M  V  S  L  A  A  L  80
TGGGAGGCCCACGGGGTGCGGCCGGCCGCGGTCGTGGGCCACTCCCAGGGCGAGGTGGCC 300
W  E  A  H  G  V  R  P  A  A  V  V  G  H  S  Q  G  E  V  A  100
GCGGCCTGCGTGGCCGGTGCCCTGTCGCTGGACGACGCTGCCCTGGTGATCGCCGGACGC 360
A  A  C  V  A  G  A  L  S  L  D  D  A  A  L  V  I  A  G  R  120
AGCAGGCTGTGGGGGCGGCTGGCCGGGAACGGCGGGATGCTCGCGGTGATGGCTCCGGCC 420
S  R  L  W  G  R  L  A  G  N  G  G  M  L  A  V  M  A  P  A  140
GAGCGGATCCGTGAGCTGCTCGAACCATGGCGGCAGCGGATTTCGGTGGCGGCGGTCAAT 480
E  R  I  R  E  L  L  E  P  W  R  Q  R  I  S  V  A  A  V  N  160
GGCCCCGCCTCGGTCACCGTCTCCGGTGACGCGCTCGCGCTGGAGGAGTTCGGCGCGCGG 540
G  P  A  S  V  T  V  S  G  D  A  L  A  L  E  E  F  G  A  R  180
CTCTCCGCCGAGGGGGTGCTGCGCTGGCCGCTGCCGGGCGTCGACTTCGCCGGCCACTCG 600
L  S  A  E  G  V  L  R  W  P  L  P  G  V  D  F  A  G  H  S  200
CCGCAGGTGGAGGAGTTCC GC5CTGAGCTCCTGGACCTGCTCTCCGGCGTACGGCCGGC 660
P  Q  V  E  E  F  R  A  E  L  L  D  L  L  S  G  V  R  P  A  220
CCTTCGCGGATACCTTTCTTCTCCACCGTGACGGCGGGTCCTTGCGGCGGCGACCAGCTG 720
P  S  R  I  P  F  P  S  T  V  T  A  G  P  C  G  G  D  Q  L  240
GACGGGGCGTACTGGTACCGCAACACGCGCGAACCCGTGGAGTTCGACGCCACGGTCCGG 780
D  G  A  Y  W  Y  R  N  T  R  E  P  V  E  F  D  A  T  V  R  260
GCGCTGCTGCGTGCGGGCCATCACACGTTCATCGAGGTCGGTCCGCATCCGCTGCTCAAC 840
A  L  L  R  A  G  H  H  T  F  I  E  V  G  P  H  P  L  L  N  280
GCCGCGATCGACGAGATCGCAGCGGACGAGGGGGTAGCGGCCACGGCCCTGCATACGCTC 900
A  A  I  D  E  I  A  A  D  E  G  V  A  A  T  A  L  H  T  L  300
CAGCGGGGCGCTGGCGGCCTTGACCGCGTGCGCAACGCGGTGGGCGCCGCTTTCGCGCAC 960
Q  R  G  A  G  G  L  D  R  V  R  N  A  V  G  A  A  F  A  H  320
GGTGTCCGGGTCGACTGGAACGCCCTGTTCGAGGGCACCGGTGCGCGCAGGGTGCCGCTT 1020
G  V  R  V  D  W  N  A  L  F  E  G  T  G  A  R  R  V  P  L  340
CCCTCGTACGCCTTC                                                1035
P  S  Y  A  F                                                  345
```

FIG. 41

PCR OLIGOS:



PCR CLONING:

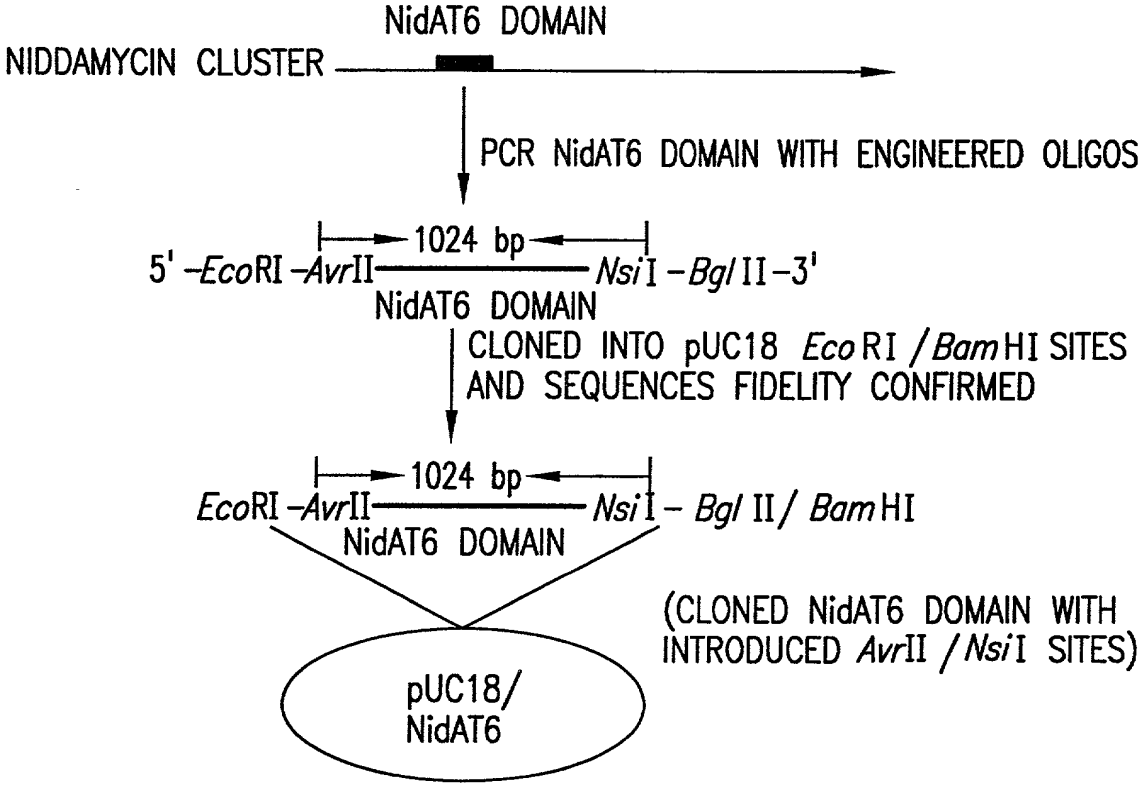


FIG.42

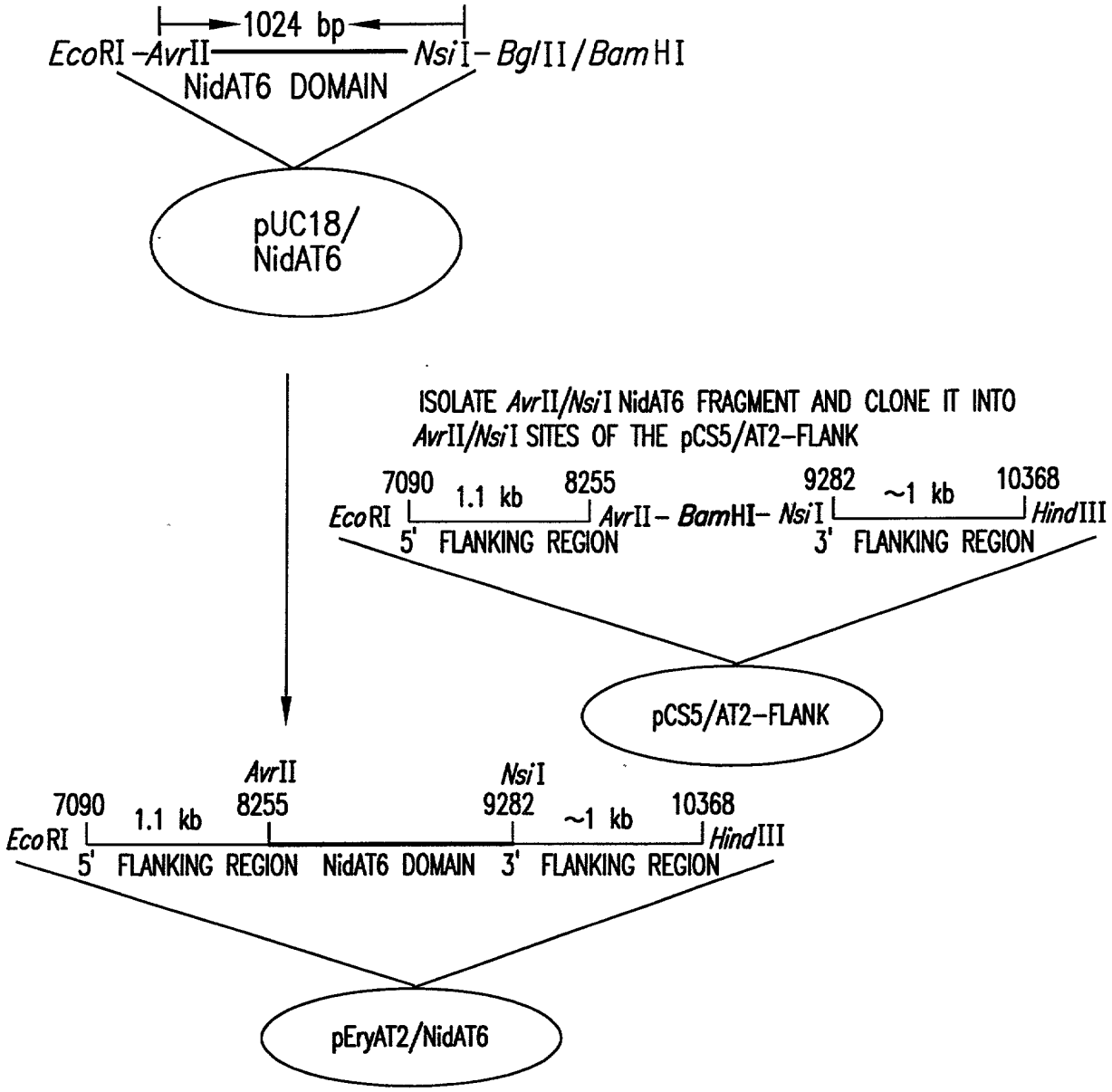

1024 bp
EcoRI -AvrII- NsiI- BglII/BamHI
NidAT6 DOMAIN
pUC18/
NidAT6
ISOLATE AvrII/NsiI NidAT6 FRAGMENT AND CLONE IT INTO
AvrII/NsiI SITES OF THE pCS5/AT2-FLANK
7090
1.1 kb
8255
9282
~1 kb
10368
EcoRI
AvrII- BamHI- NsiI
HindIII
5' FLANKING REGION
3' FLANKING REGION
pCS5/AT2-FLANK
AvrII
NsiI
7090
1.1 kb
8255
9282
~1 kb
10368
EcoRI
HindIII
5' FLANKING REGION
NidAT6 DOMAIN
3' FLANKING REGION
pEryAT2/NidAT6

FIG.43